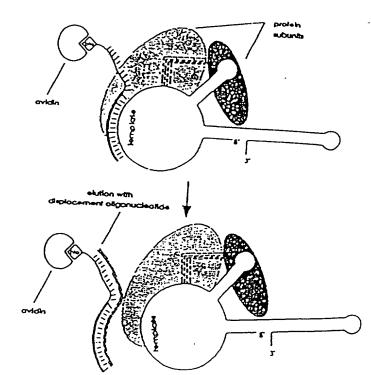
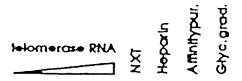
Attorney Docket No. 015389-002990US In re: Cech et al.

Application No.: To be assigned Filed: January 18, 2002 For: NOVEL TELOMERASE





PANEL B



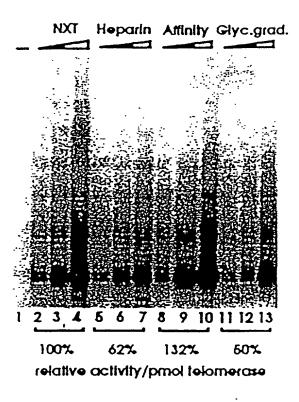


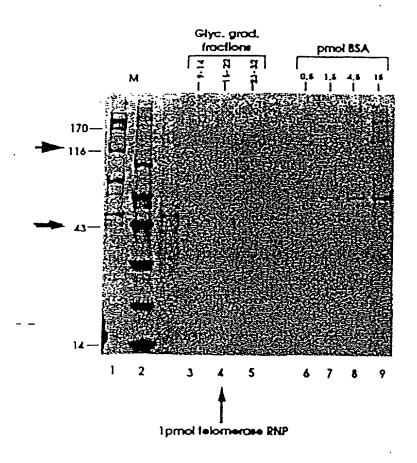


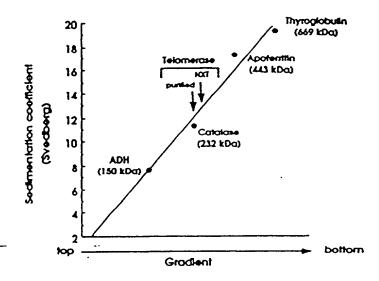
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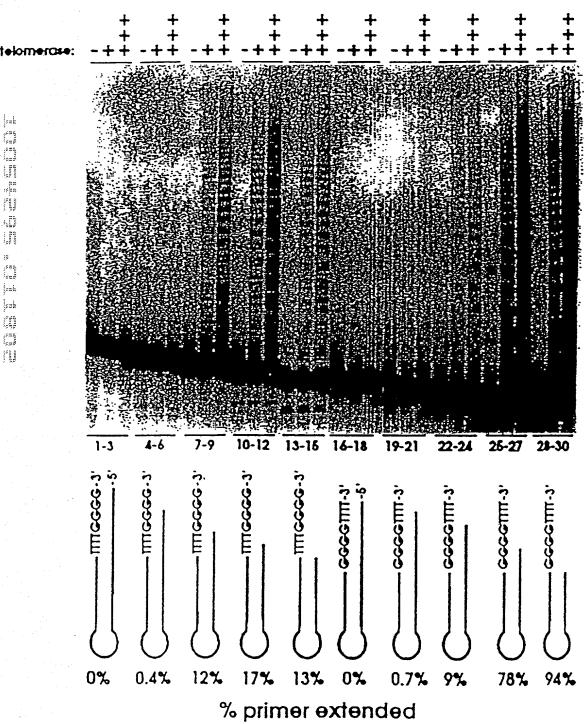


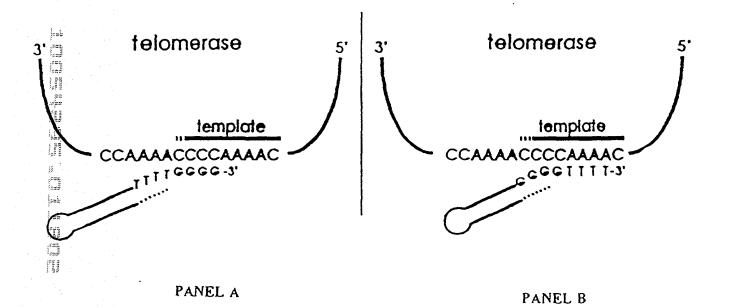


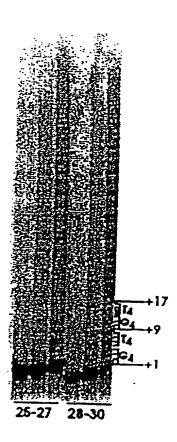
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1 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT 51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA 101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC 151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA 201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT 251 TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG 301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT 351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACTTCTT 401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTCA 451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA 501 CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG 551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA 601 GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG 651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA 701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA 751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA 801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT 851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTC 901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA 951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG 1001 CTTGAGAAAG TCAAAGATTT TAACTTCAAC TACTATTTAA CAAAATCTTG 1051 TCCTCTTCCA GAAAATTGGC GGGAACGGAA ACAAAAAATC GAAAACTTGA 1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC 1151 TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA 1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC 1251 AAAAGAAAGT TAAGAAATAT GTGGAACTAA ACAAGCATGA ACTCATTCAC 1301 AAAAACTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA 1351 GGTTGAGACC TCTGCAAAGC ATTTTTATTA TTTTGATCAC GAAAACATCT 1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG 1451 CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA 1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA 1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT 1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT 1651 ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG 1701 TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC GAAGTTATTG 1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC 1801 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG 1851 AGTTTGTTTG CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTTGCA 1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAACTATC 1951 AACATTCCTA AAAACTACTA AATTACTTTC TTCAGATTTC TGGATTATGA 2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC 2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT 2101 TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG 2201 AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG 2251 CCAATATAAT TACATTAACT TTAATGGGAA GTTTTATAAA CAAACAAAAG 2301 GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTCATC ATTTTATTAT

FIGURE 9 (cont.)

2351	GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA
2401	CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC
2451	TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT
2501	ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAAACTACA
2551	GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA
2601	GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC
2651	TCAATTGATA TGAAAACTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT
2701	AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT
2751	CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC
2801	CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCGA ATAAAACTCT
2851	CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG
2901	AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG TATGATCGAC
2951	TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
3001	CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG
3051	ACTITITCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA
3101	AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA
3151	GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA
3201	CTATTCTAAC TTATTTTGGA AAGTTAATTT TCAATTTTTG TCTTATATAC
3251	TGGGGTTTTG GGGTTTTGGG GTTTTGGGG

- 1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIOKVIRC RNOSOSHYKD
- 51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL
- 101 SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM
- 151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGA
- 201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNNMKSRTR IFYCTHFNRN
- 251 NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKKLK DKVIEKIAYM
- 301 LEKVKDFNFN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS
- 351 YTTDNKCVTO FINEFFYNIL PKDFLTGRNR KNFOKKVKKY VELNKHELIH
- 401 KNLLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKLL RWIFEDLVVS
- 451 LIRCFFYVTE QQKSYSKTYY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV
- 501 EEWKKSLGFA PGKLRLIPKK TTFRPIMTFN KKIVNSDRKT TKLTTNTKLL
- 551 NSHLMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK OVGOPKLFFA
- 601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVIDSKN
- 651 FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKTLIVEAKQ
- 701 RNYFKKDNLL OPVINICOYN YINFNGKFYK OTKGIPOGLC VSSILSSFYY
- 751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVLFIEKL
- 801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI
- 851 SIDMKTLALM PNINLRIEGI LCTLNLNMQT KKASMWLKKK LKSFLMNNIT
- 901 HYFRKTITTE DFANKTLNKL FISGGYKYMQ CAKEYKDHFK KNLAMSSMID
- 951 LEVSKIIYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK
- 1001 KYIFNRVCMI LKAKEAKLKS DQCQSLIQYD A

1751 GGGGTTTTGG GG

FIGURE 11

1 CCCCAAAACC CCAAAACCCC AAAACCCCTA TAAAAAAAGA AAAAATTGAG 51 GTAGTTTAGA AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA 101 TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA 151 GCTCTTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA 201 TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT 251 CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA 301 AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA 351 AATCAGGTAA TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA 401 TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTTC 451 CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG 501 GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG 551 AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCG 601 TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC 651 TTGAGACAAT TGAAAAAGCT GTTTACAACT GAAGGAATCG CAGTTCTGAA 701 AGTTCTGATG TGTATGCCAT TATTTTGTGA ATTAATCTCA AATATCTTAT 751 CTCAATTTAA TGGATAGCTA TAGAAACAAA CCAAATAAAC CATGCAAGTT 801 TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC TGAATTTATA 851 TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC 901 TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT 951 AAAAGAAGCA GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT 1001 TTGTTGATTC TTCTGTAACC GGAATTAACA ACAAGAATAT TAGCAACGAA 1051 AAAGAAGAAG AGCTATCACA ATCCTGATTC TTAAAGATTT CAAAAATTCC 1101 AGGTAAGAGA GATACATTCA TTAAAATTCA TATATTATAG TTTTTCATTT 1151 CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA 1201 GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT 1251 TCACATTCAT AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA 1301 GCAGTCATCC GTTTTAAAAA TAGTGCTATG AGGACTAAAT TTTTAGAGTC 1351 AAGAAATGGA GCCGAAATCT TAATCAAAAA GAATTGCGTC GATATTGCAA 1401 AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA ATCTTGATTG 1451 ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATTA AAGAAATAAA 1501 GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG 1551 CGĀTCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAA 1601 ATACAAACCT TGGTCAAAAT ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA 1651 AAAGAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA

1701 AAGATTTATT TTTTTCAATA ATTTATTGAA AAGAGGGGTT TTGGGGTTTT

		CCCCAAAACCCCAAAACCCCTATAAAAAAAAAAAAAATTGAGGTAGTTTAGA	
		GGGGTTTTGGGGTTTTGGGGATATTTTTTTTTTTTTAACTCCATCAAATCT	60
a b c	E	PQNPKTPKPL * KKKKLR * FR PKTPKPQNPYKKRKNCGSLE PKPQNPKTPIKKEKIEVV * K	- -
	61	AATAAAATATTATTCCCGCACAAATGGAGATGGATATTGATTTGGATGATATAGAAAATT	
		TTATTTATAATAAGGGCGTGTTTACCTCTACCTATAACTAAACCTACTATATCTTTTAA	120
a b ⊭ c	N	I K I L F P H K W R W I L I W M I. * K I I K Y Y S R T N G D G Y C F G C Y R K F * N I I ? A Q M E M D I D L D D I E N L	-
Tuni	121	TACTTCCTAATACATTCAACAAGTATAGCAGCTCTTGTAGTGACAAGAAAGGATGCAAAA	100
r (freez)		${\tt ATGAAGGATTATGTAAGTTGTTCATATCGTCGAGAACATCACTGTTCTTTCCTACGTTTT}$	180
a b c	Y	FLIHSTSIAALVVTRKDAK TS*YIQQV*QLL**QERMQN LPNTFNKYSSSCSDKKGCKT	-
gan.	181	CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG	240
:		${\tt GTAACTTTAGACCGAGCTTTAGCGGAAGTAACTGATAAGGTTTCAACGTTTTTGTTAATC}$	210
a b c	н	CNLARNRLHCLFQSCKNN. IEIWLEIAFIDYSKVAKTIR LKSGSKSPSLTIPKLQKQLK	- - -
1444	241	AGTTCTACTTCTCGGATGCAAATCTTTATAACGATTCTTTCT	
and a		TCAAGATGAAGAGCCTACGTTTAGAAATATTGCTAAGAAAGA	300
a b c	S	STSRMQIFITILSCEN·F· VLLLGCKSL·RFFLEKISFK FYFSDANLYNDSFLRKLVLK	-
	301	AAAGCGGAGAGCAAAGAGTAGAAATTGAAACATTACTAATGTTTAAATAAA	
	301	TTTCGCCTCTCGTTTCTCATCTTTAACTTTGTAATGATTACAAATTTATTT	360
a b c	K !	A E S K E ' K L K H Y ' C Ł N K I R · K R A K S R N C N I T N V · I K S G N G G G G G G G G G G G G G G G G G	-
	361 -	TGAGGATTATTCTATTTTTTAGATCACTTCTTAAGGAGCATTATGGAGAAAATTACTTAA	
		ACTCCTAATAAGATAAAAAATCTAGTGAAGAATTCCTCGTAATACCTCTTTTAATGAATT	426
a b c	C	CLFYFLDHFLRSIMEKIT. EDYSIF.ITS.GALWRKLLN RIILFFRSLLKEHYGENYLI	- - -
	421 -	TACTAAAAGGTAAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTAAATT	
		ATGATTTTCCATTTGTCAAACCTAATAAAGGGATCGGTTGTTACTACTCATATAATTTAA	480
a b c	Y	· K V N S L D Y F P S Q Q C C V Y · I F K R · T V W I I S L A N N D E Y I K F L K G K Q F G L F P · P T M M S I L N S	- -

FIGURE 12 (cont.)

	481	CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT GTATACTCTTACTCAGTTTCCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA	540
a b c	ŀ	H M R M S Q R I S I H Q T Y Q R Q T R Y I C E C V K G S R Y I R L T K D K L A I Y E N E S K D L D T S D L P K T N S L	- - -
	541	AAAACGCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATTGCATTTACTATTCG TTTTGCGTTCTTTTTCAAACTATTAGCTTGTCGTCTTCTTGAATAACGTAAATGATAAGC	600
a b c	. 1	T Q E K V C * S N S R R T Y C I Y Y S K R K K K F D N R T A E E L I A F T I R N A R K S L I I E Q Q K N L L H L L F V	<u>-</u> -
	601	TATGGGTTTTATTACAATTGTTTTAGGTATCGACGGTGAACTCCCGAGTCTTGAGACAAT ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA	660
a b c	Y	G F Y Y N C F R Y R R C T P E S C D N . M G F I T I V L G I D G E L P S L E T I W V L L Q L F * V S T V N S R V L R Q L	- -
North Track	661	TGAAAAAGCTGTTTACAACTGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT ACTTTTTCGACAAATGTTGACTTCCTTAGCGTCAAGACTTCAAGACTACACATACGGTA	720
a b c		CKSCLQLKESQFCKF * CVCH EKAVYNCRNRSSESSDVYAI KKLFTTEGIAVLKVLMCMPL	-
tudh Besst Baus	721	TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA ATAAAACACTTAATTAGAGTTATAGAATAGA	780
a b comp	Y	F V N S Q I S Y L N L M D S Y R N K I L C I N L K Y L I S I * W I A I E T N F C E L I S N I L S Q F N G * L * K Q T	-
Section 2	781	CCAAATAAACCATGCAAGTTTAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCCTGTTTACGTGTG	840
a b	· F	PNKPCKFNGIYVKSFGTNAH QINHASLMEYTLNPLGQMHT K·THQV·WNIR·ILWDKCTL	- -
	841	TGAATTTATATTGGATTCTTAAAGCATAGATACACAGAATGCTTTAGAGACTGATTTAGC ACTTADATATAACCTAAGAATTTCGTATCTATGTGTCTTACGAAATCTCTGACTAAATCG	900
a b c	c	TIYIGFLK HRYTECFRDCFS EFILDS TSIDTQNALETD'LA NLY%!LKATIHRML TRLITL	-
		TTACAACAGATTACCTGTTTTGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA AATGTTGTCTAATGGACAAAACTAATGAGAACGAGTAGAGAATATAGAAATTTTCTTCGT	960
a b c		. Q Q I T C F D Y S C S S L I S L K E A Y N R L P V L I T L A H L L Y L * K K Q T T D Y L F C L L L I S Y I F K R S R	
	961	GGCGAAATGAAAGAAGACTAAAGAAAGAGATTTCAAAATTTGTTGATTCTTCTGTAACC CCGCTTTACTTTTCTTCTGATTTCTTTCTCTAAAGTTTTAAACAACTAAGAAGACATTGG	1020
a b c		E M K R R L K K E I S K F V D S S V T A K C K E D · R K R F Q N L L I L L · P R N E K K T K E R D F K I C C F F C N R	-
	1021	GGAATTAACAACAAGAATATTAGCAACGAAAAAGAAGAAGAGCTATCACAATCCTGATTC CCTTAATTGTTGTTCTTATAATCGTTGCTTTTTTCTTCTTCTCGATAGTGTTAGGACTAAG	1080
a b c		ELTTRILATKKKKSYHNPDS N-QQEY-OPKRRRAITILIL	-

FIGURE 12 (cont.)

	1081	TTAAAGATTTCAAAAATTCCAGGTAAGAGAGATACATTCATT	
a b c		L K I S K I P G K R D T F I K I H I L ° - R F Q K F Q V R E I H S L K F I Y Y S - K D F K N S R * E R Y I H * N S Y I I V -	
	1141	TTTTTCATTTCACAGCTGTTATTTTCTTTTATCTTAACAATATTTTTTGATTAGCTGGAA	
a b c		FFISQLLFSFILTIFFD * LE - FSFHSCYFLLS * QYFLISWK - FHFTAVIFFYLNNIFCLAGS -	
		GTAAAAAGTATCAAATAAGAGAAGCGCTAGACTGAGGTAACTTAGCTTATTCACATTCAT	
	1201	CATTTTCATAGTTTATCCTCTCGCGATCTGACTCCATTGAATCGAATAAGTGTAAGTA	
a b c		V K S I K * E K R * T E V T * L I H I H - K V S N K R S A R L R * L S L F T F I - K K Y Q I R E A L D C G N L A Y S H S * -	
A H H H H H H H H H H H H H H H H H H H	1261	AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTTAAAAA 1320 TCTAGCTGGAAGTATATAGGTTATGCTACTATTCCTTTGTCGTCAGTAGGCAAAATTTTT	
ab C		R S T F I Y P I R C * G N S S H P F * K - D R P S Y I Q Y D D K E T A V I R F K N - I D L H I S N T M I R K Q Q S S V L K I -	
### ###		TAGTGCTATGAGGACTAAATTTTTAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAAA	
A House	1321	ATCACGATACTCCTGATTTAAAAATCTCAGTTCTTTACCTCGGCTTTAGAATTAGTTTTT	
a b c		* C Y E D * I F R V K K W S R N L N Q K - S A H R T K F L E S R N G A E I L I K K - V L C G L N F * S Q E H E P K S * S K R -	
	1381	GAATTGCGTCGATATTGCAAAAGAATCGAACTCTAAATCTTTCGTTAATAAGTATTACCA	
a b C		ELRRYCKRIEL IFR VLP - NCVDIAKESNSKSFVNKYYQ - IASILQKNRTLNLSLISITN-	
	1441	ATCTTGATTGATGAAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAAGAAATAAA 1500 TAGAACTAACTACTTCTTAACTGCTCCGTTGACGTGTCTTCTAGTAATTTCTTTATTT	
a b c		I L I D C R D * R G N C T E D H * R N K - S C L I E E I D E A T A Q K I I K E I K - L D C L K R L T R Q L H R R S L K K * S -	
	1501	GTAACTTTTATTAATTAGAGAATAAACTAAATTACTAATATAGAGATCAGCGATCTTCAA	
a b c		V T F I N ' R I N ' I T N I E I S D L Q - L L L I R E ' T K L L I ' R S A I F N - N F Y ' L E N K L N Y ' Y R D Q R S S I -	
		TTGACGAAATAAAAGCTGAACTAAAGTTAGACAATAAAAAAATACAAACCTTGGTCAAAAT	
a b c		LTK * KLN * S * T I KNT N L G Q N - C R N K S C T K V R Q * K I Q T L V K I - D E I K A E L K L D N K K Y K P W S K Y -	
		ATTGAGGAAGGAAAAGAACCAGTTAGCAAAAGAAAAAATAAGGCAATAAATA	
	1621	TAACTCCTTCCTTTTCTTCTGGTCAATCGTTTTTTTTTT	
a b c		I E E G X E D Q L A K E K I R O · ! K C · L R K E X K T S · Q K K K · G N X · N E · C C R X R P V S K R X N X A I N K M S ·	

FIGURE 12 (cont.)

	GTACAGAAGTGAAGAAATAAAGAGTTTATTTTTTCAATAATTTATTGAAAAGAGGGGTT 1681								1740																
		CAT	6161	ICA	_ 1 1	CII	IMI	111	CIA	AA	·AA		A.A.	1 G1-	TAT	"L'A	LAA	TAA	C1	1-1-1	CT		CAA	,	
а		v o	к	c	R	N	К	R	F	ı	F	-	F	N	N		L	L	ĸ	R	. (3	v	_	
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		TTGG	GGTT	TTG	GGG	TTT	TGG	GG																	
	1741			- +		-	+		176	2															
		AACC	CCAA	AAC	CCC	AAA	ACC	CC																	
a b		L G	F 3 F	W G	G V	F L	G		-																

2	EVDVD:NOADNHGIHSALKTCEEIKEAKTLYSWIQKVIRCRNQSQSHYKDL	51
19	ELELEMQENONDIQVRVK IDDPKQY . LVNVTAACLLQEGSYYQDK	
52	EDIX:FAQTNIVATPRDYNEEDFKVIARKEVF.STGLMIELIDKCLVELL :: :	100
63	DERRYLITKALLEVAESDPEFICQLAVYIRNELYIRTTTNYIVAF.	107
101	SSSDVSDRQKLQCFGFQLKGNQLAKTHLUTALSTQKQYFFQDEWNQVRAM:: : : : : : : : : : : : : :	150
151	IGNELFRHLYTKYLI FQRTSEGTLVQFCGNNVFDHLKVNDKFDKKQKGGA	200
	::. : : ::: . :: :: :: :: :: :: :: :: :: :: :: :: ::	181
201	ADMNE PRCCSTCKYNVKNEKDHFLNNINVPNWNNMKSRTRIFYCTHF	247
182	SEFNEYOLGKYCTES QRKKTMFRYLSVTNKQKWDQTKKK	220
248	NRNNOFFKKHEFVSNKNNISAMDRAQTIFTNIFRFNRIRKKLKDKVIEKI	297
221	: · : . : : 	264
298	AYMLEKVKDFNFNYYLTKSCPLPENWRERKOKIENLINKTREEKSKYYEE	347
265	AKRONAMK KHMKAPKIPNSTLESKYLTFKD	294
348	LFSYTTDNKCVTQFINEFFYNILPKDFLTGRNRKNFQKKVKKYVELNKHE	397
295	LIKFCHISEP KERVYKILGKKYPKTEEEYKAAFGDSASAPFN.PE	338
	LIHKNLLLEKINTREISWMQVETSAKHFYYFDHENIYVLWKLLRWIFEDL : . : . : : . : : : LAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSN	386
	VVSL:RCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSIADLKKETLAEVQE	497
387	: :: : :: : ::	394
498	KEVEEWKKSLGFAPGKLRLIPKKTTFRPIMTFNKKIVNSDRKTTKLTTNT	547
395	: 	398
548		597
399	IVINK :	415
598	FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKNNIVID	647
416	F .PLOFFSAIEAVN .EAVTKGFKAKK RENMNLKGQIEAVKE	457
	SKNFRKKEMKDYFRQKFQKIALEGGQYPTLFSVLENEQNDLNAKKTLIVE .	697
	KTDEEKKOMELEQTEEGEFVKVNEGIGKQYINSIELAIK	496
	AKQRNYFKKDNLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSS	
	IAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGAKKYGSVRTCLECALVLGL	
	FYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLITTQENNAVLFI : : : : : : : : : : : : : : : : :	
	EKLINVSRENGFKFNMKK.LQTSFPLSPSKFAKYGMDSVEEQNIVQDYCD	
577		617
847	wigisidmxtlalmpninlriegilctlnlnmqtkkasmwlkkklksflm	896
618	-	653
897	NNITHYFRKTITTEDFANKTLNKLFISGGYKYMQCAKEYKD HFKKNLAM	945
654	: : : ::: :: :: :: PNIKIF AVDLEGYG	687
946 I	SSMIDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFIE	995
	. : :: . : : :: SDSILKFISAKQGGAMMVE	706
:	: ::::::::::::::::::::::::::::::::::	

	LSTQKQTFFQDEWMQVRAMIGNEE.FRHLTTKTLIFQKTSEGTLVQFC 	43
179		228
44	:::: ::::	84
229	VPNWNNHKSRTRIFYCTHFNRNNOFFKKHEFVSNKNNISAMDRAQTIFTN	278
85		114
279	IFRFNRIRKKLKDKVIEKIAYMLEKVKDFNFNYYLTKSCPLPENWRERKQ	328
115	GLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRRETDY	164
329		377
165		200
378	RNRKNFQKKVKKYVELNKHELIHKNLLLEKINTREISWMQVETSAKHFYY	427
201		242
428		475 290
476	WDVIHKHSIADLKKETLAEVQEKEVEEWKKSLGFAPGKLRLIPKKTTFRP	525
291	: :: : : : : : : : . : 	330
526	INTFNKKIVNSDRKTTKLTTNTKLLNSHLMLKTLKNRMFKDPFGFAVFNY	575
331	VYSFSTDLKLVD. TNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENL	378
576 379	: :: :: :: :: :: :: :: :: :: :: :: ::	615 426
516	LSTFL KTTKLLSSDFWIMTAQILKRKNNI. VIDSKNFRKKEMK	657
427	:	476
558	DYFRQKFQKIALEGGQYPTLFSVLEN EQNDLNAKKTLIVEAKQRNYFK	705
477	EETPETKDETPSESTSCHKFFDHLSELTELEDFSVN LQATQEIY	520
706	KDNELOPVINICOYNYINFNGKFYKOTKGIPOGLCVSSILSSFYYATLEE	755
521	DSLHKLLIRSTNIKKFKLSYKYEMEKSKMDTFIDLKNIYETLIN	564
756	SSLGFLRDESHNPENPNVNLLMRLTDDYLLITTQENNAVLFIEKLINVSR	905
565	LKRCSVNISNPHGNISYELTNKDSTFYKFKLTLNQE	500
	ENGFKFNMKKLOTSFPLSPSKFAKYGMDSVEEQNIVQDYCDWIGISIDMK	
501		648 901
649	.:	691
902		948
692	:	741
949		982
742		791
983	PDFFLS TLEMFIEIFSTKKY IFNRVCHILKAKEAKLKSDQCQSLIQ 1	028
792	DONTVSDDSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLK 8	10

	DIDLDDIENLLPNTFNKYSSSCSDKKGCKTLKSGSKSPSLTIPK	
48	LOKOLEFYFSDANLYNDSFLRKLVLKSGEORVEIETLLM : : : ::: :: ::	86
667	FNKPNLLFFKQFEQLKNLENVSINCILDQHILNSISEFLEKNKKIKAFIL	716

1	MEMDIDLDDIENL. LPNTFNKYSSSCSDKKGCKTLKSGSKSPS	42
491	IELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGAKKYGSVRTCLEC	540
	•	
43	LTIPKLQKQLEFYFSDANLYNDSFLRKLVLKSGEQRVEIETLL	85
541	ALVI CLIMOKORCEKSSEYTESSESSOCNKCYL EVOLEGDELRESMOKLI.	589

Motif A

Motif B

YOSILSSFYYATLEESSLGFL SLSPLWFCLALNPLSHQLHUDR PTSPALCNAVLLRLDRRLAGLA KGSPAIFQSSMTKILEPFRKQN A PIVD CVY DD LLE FYSEPK VLPELYPMKFDVKSCYDSIPRMECMRILKDALKN- 68-RCYIREOGLFNESSL GQPKLFPATMEI EKCYDSVNREKLSTFLKTTKLL-100-KFYRQTKGI F 7-SIRYQYNVLP 26-HVPVGPRVCV 28-RQLAIKKGIY VGDAYF SVPLDEDFRKYTAFTIP-YKKAFDSIPHSWLIQVLEIYKIN-LKKCFDTISHDLIIKELKRYISDh--h---h---h KNRNLHCTYI al S.c.(groupII)FGGSNWFREW LKACK SVTVI p123 L8543.12 years Dong (LINE) telomerase Consensus HIV-RT

Hotif C

Motif D

Motif B

dy-h 市 20 55-YVRYADDILIGVLGSKW-2-KIIKRDLNNFLNS.IGLTINEERILI- 4-ETPARFLGYNI 4-IYQYMDDLYVGSHLEIG-1-HRTKIBELRQHLLRWGLTTPDRKHQK- 0-EPPFLWMGYEL 8-ILKLADDFLIISTDQQQ....VINIKKLAMGGRQKYNAKANR-41-IRSKSSKGIFR 나-나 DYLLITTQENN-0-AVLFIEKLINVSREN<mark>GFKFNMM</mark>KQT-23-QDYCDMI en-h---10 X X Y AKNDKE - 0 - MKKL I DTTT I FSND ISMQPGLE निरम h----16-HLIYM -55-YVRYA -14-LMBLT al S.c. (groupII) telomerase pl23 T Z > Dong (LINE) Consensus L8543.12 HIV-RT

telomerase p43 human La Xenopus LaA Drosophila La S. c. Lhplp

Mary as a series of the series

LQKOLEFYESDANLYNDSFLRKLVLKSGEQRVEIETLLM ICHOLEYYEGDFNLPRDKFLKEQI.KLDEGWYPLEIMIK ICEOIEYYEGDANLNRDKFLKQQI.LLDDGWYPLETMIK ILROVEYYEGDANLNRDKFLREQIGKNEDGWYPLSVLVT CLKOMEFYESEFNFPYDRELRTTAEK.NDGWYPISTIAT

2401 aaagaacaaa aaagattaaa a

FIGURE 19

l aactcattta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa 61 tagatttaat ttagaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata 121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga 181 tatataagtt agggttaaga ttgacgatcc taagcaatat ctcgtgaacg tcactgcagc 241 atgtttgttg taggaaggta gttactacta agataaagat gaaagaagat atatcatcac 301 taaagcactt cttgaggtgg ctgagtctga tcctgagttc atctgctagt tggcagtcta 361 cateegtaat gaactttaca teagaactae caetaactae attgtageat tttgtgttgt 421 ccacaagaat actcaaccat tcatcgaaaa gtacttcaac aaagcagtac ttttgcctaa 481 tgacttactg gaagtetgtg aatttgcata ggttetetat atttttgatg caactgaatt 541 caaaaatttg tatettgata ggataettte ataagatatt egtaaggaac teaettteeg 601 taagtgttta caaagatgcg tcagaagcaa gttttctgaa ttcaacgaat actaacttgg 661 taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttacctct cagttaccaa 721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta 781 ggcaataaag gaatetgaag ataagtecaa gagagaaaet ggagacataa tgaaegttga 841 agatgcaatc aaggctttaa aaccagcagt tatgaagaaa atagccaaga gatagaatgc 901 catgaagaaa cacatgaagg cacctaaaat tectaactet acettggaat caaagtaett 961 gaccticaag gatctcatta agttctgcca tatttctgag cctaaagaaa gagtctataa 1021 gatcettggt aaaaaatace etaagacega agaggaatac aaagcageet ttggtgatte 1081 tgcatctgca cccttcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa 1141 aacatgggaa aatgaactca gtgcaaaagg caacactgct gaggtttggg ataatttaat 1201 ttcaagcaat taactcccat atatggccat gttacgtaac ttgtctaaca tcttaaaagc 1261 eggtgtttca gatactacac actetattgt gatcaacaag atttgtgage ccaaggeegt 1321 tgagaactee aagatgttee etetteaatt etttagtgee attgaagetg ttaatgaage 1381 agttactaag ggattcaagg ccaagaagag agaaaatatg aatcttaaag gtcaaatcga 1441 agcagtaaag gaagttgttg aaaaaaccga tgaagagaag aaagatatgg agttggagta 1501 aaccgaagaa ggagaatttg ttaaagtcaa cgaaggaatt ggcaagcaat acattaactc 1561 cattgaactt gcaatcaaga tagcagttaa caagaattta gatgaaatca-aaggacacac 1621 tgcaatette tetgatgttt etggttetat gagtacetea atgteaggtg gagceaagaa 1681 gtatggttcc gttcgtactt gtctcgagtg tgcattagtc cttggtttga tggtaaaata 1741 acgttgtgaa aagteeteat tetacatett eagtteacet agtteteaat geaataagtg 1801 ttacttagaa gttgatetee etggagaega acteegteet tetatgtaaa aaettttgea 1861 agagaaagga aaacttggtg gtggtactga tttcccctat gagtgcattg atgaatggac 1921 aaagaataaa actcacgtag acaatatcgt tattttgtct gatatgatga ttgcagaagg 1981 atattcagat atcaatgtta gaggcagttc cattgttaac agcatcaaaa agtacaagga 2041 tgaagtaaat cctaacatta aaatctttgc agttgactta gaaggttacg gaaagtgcct 2101 taatctaggt gatgagttca atgaaaacaa ctacatcaag atattcggta tgagcgattc 2161 aatettaaag tteattteag eeaageaagg aggageaaat atggtegaag ttateaaaaa 2221 ctttgccctt caaaaaatag gacaaaagtg agtttcttga gattcttcta taacaaaaat 2281 ctcaccccac ttttttgttt tattgcatag ccattatgaa atttaaatta ttatctattt 2341 atttaagtta cttacatagt ttatgtatcg cagtctatta gcctattcaa atgattctgc

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL

VNVTAACLLQEGSYYQDKDERRYIITKALLEVAESDPEFICQLAVYIRNELYIRTTTN

YIVAFCVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYIFDATEFKNLYLDRILS

QDIRKELTFRKCLQRCVRSKFSEFNEYQLGKYCTESQRKKTMFRYLSVTNKQKWDQTK

KKRKENLLTKLQAIKESEDKSKRETGDIMNVEDAIKALKPAVMKKIAKRQNAMKKHMK

APKIPNSTLESKYLTFKDLIKFCHISEPKERVYKILGKKYPKTEEEYKAAFGDSASAP

FNPELAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNILKAGV

SDTTHSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKRENMNLKGQIE

AVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIGKQYINSIELAIKLAVNKNLDEIKG

HTAIFSDVSGSMSTSMSGGAKKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQ

CNKCYLEVDLPGDELRPSMQKLLQEKGKLGGGTDFPYECIDEWTKNKTHVDNIVILSD

MMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKIFAVDLEGYGKCLNLGDEFNENNYI

KIFGMSDSILKFISAKQGGANMVEVIKNFALQKIGQK

l tcaatactat taattaataa ataaaaaaaa gcaaactaca aagaaaatgt caaggcgtaa 61 ctaaaaaaag ccataggctc ctataggcaa tgaaacaaat cttgattttg tattacaaaa 121 tetagaagtt tacaaaagee agattgagea ttataagaee tagtagtaat agateaaaga 181 ggaggatete aagettttaa agtteaaaaa ttaagattag gatggaaact etggeaacga 241 tgatgatgat gaagaaaaca actcaaataa ataataagaa ttattaagga gagtcaatta 301 gattaagtag caagtttaat tgataaaaaa agttggttct aaggtagaga aagatttgaa 361 tttgaacgaa gatgaaaaca aaaagaatgg actttctgaa tagcaagtga aagaagagta 421 attaagaacg attactgaag aataggttaa gtattaaaat ttagtattta acatggacta 481 ccagttagat ttaaatgaga gtggtggcca tagaagacac agaagagaaa cagattatga 541 tactgaaaaa tggtttgaaa tatctcatga ccaaaaaaaat tatgtatcaa tttacgccaa 601 ctaaaagaca tcatattgtt ggtggcttaa agattatttt aataaaaaca attatgatca 661 tettaatgta ageattaaca gaetagaaac tgaageegaa ttetatgeet ttgatgattt 721 ttcacaaaca atcaaactta ctaataattc ttactagact gttaacatag acgttaattt 781 tgataataat ctctgtatac tcgcattgct tagattttta ttatcactag aaagattcaa 841 tattttgaat ataagatctt cttatacaag aaattaatat aattttgaga aaattggtga 901 getaettgaa actatetteg eagttgtett tteteatege eaettaeaag geatteattt 961 acaagtteet tgegaagegt tetaatattt agttaaetee teateataaa ttagegttaa 1021 agatagetaa ttataggtat actetttete tacagactta aaattagttg acactaacaa 1081 agtccaagat tattttaagt tettataaga atteeetegt ttgactcatg taagetagta 1141 ggctatccca gttagtgcta ctaacgctgt agagaacctc aatgttttac ttaaaaaggt 1201 caagcatgct aatcttaatt tagtttctat ccctacctaa ttcaattttg atttctactt 1261 tgttaattta taacatttga aattagagtt tggattagaa ccaaatattt tgacaaaaca 1321 aaagettgaa aatetaettt tgagtataaa ataateaaaa aatettaaat ttttaagatt 1381 aaacttttac acctacgttg cttaagaaac ctccagaaaa cagatattaa aacaagctac 1441 aacaatcaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa ctaaagatga 1501 aactecaage gaaageacaa gtggtatgaa attttttgat catetttetg aattaacega 1561 gettgaagat tteagegtta aettgtaage taeceaagaa atttatgata gettgeacaa 1621 acttttgatt agatcaacaa atttaaagaa gttcaaatta agttacaaat atgaaatgga 1681 aaagagtaaa atggatacat tcatagatct taagaatatt tatgaaacct taaacaatct 1741 taaaagatgc tetgttaata tateaaatee teatggaaac atttettatg aactgacaaa 1801 taaagattet aettittata aatttaaget gaeettaaae taagaattat aacaegetaa 1861 gtatactttt aagtagaacg aattttaatt taataacgtt aaaagtgcaa aaattgaatc 1921 ttecteatta gaaagettag aagatattga tagtetttge aaatetattg ettettgtaa 1981 aaatttacaa aatgttaata ttategeeag tttgetetat eecaacaata tttagaaaaa 2041 teettteaat aageeeaate ttetatttt eaageaattt gaataattga aaaatttgga 2101 aaatgtatet ateaaetgta ttettgatea geatataett aattetattt eagaattett 2161 agaaaagaat aaaaaaataa aagcattcat tttgaaaaga tattatttat tacaatatta 2221 tettgattat actaaattat ttaaaacact teaatagtta eetgaattaa attaagttta 2281 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaaa 2341 ccacaagcaa aaagctttct atgaaccatt atgtgagttt atcaaagaat catcctaaac 2401 cetttageta atagattttg accaaaacae tgtaagtgat gaetetatta aaaagatttt 2461 agaatetata tetgagteta agtateatea ttatttgaga ttgaaceeta gttaatetag 2521 cagtttaatt aaatctgaaa acgaagaaat ttaagaactt ctcaaagctt gcgacgaaaa 2581 aggigittia giaaaagcat actataaatt ccctctatgt tiaccaactg giacttatta 2701 tgaatattic titigettatt attigaataa tacatacaat agicattitt agigttitga 2761 atatatttta gitatttaat teattattit aagtaaataa tiattittea ateattitti 2821 aaaaaatcg

MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQQIK EEDLKLLKFKNQDQDGNSGNDDDDEENNSNKQQELLRRVNQIKQQVQLIKKVGSKVEK DLNLNEDENKKNGLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRR ETDYDTEK WFEISHDQKNYVSIYANQKTSYCWWLKDYFNKNNYDHLNVSINRLETEAE FYAFDDFSQTIKLTNNSYQTVNIDVNFDNNLCILALLRFLLSLERFNILNIRSSYTRN OYNFEKIGELLETIFAVVFSHRHLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQVYSF STDLKLVDTNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNL USIPTQFNFDFYFVNLQHLKLEFGLEPNILTKQKLENLLLSIKQSKNLKFLRLNFYTY VAQETSRKQILKQATTIKNLKNNKNQEETPETKDETPSESTSGMKFFDHLSELTELED FSVNLQATQEIYDSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLK RCSVNISNPHGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFNNVKSAKIE SSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNPFNKPNLLFFKQFEQLK NLENVSINCILDQHILNSISEFLEKNKKIKAFILKRYYLLQYYLDYTKLFKTLQQLPE LNOVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDFDQNTVSD DSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLKACDEKGVLVKAYYKFP LCLPTGTYYDYNSDRW

MKILFEFIQDKLDIDLQTNSTYKENLKCGHFNGLDEILTTCFAL PNSRKIALPCLPGDLSHKAVIDHCIIYLLTGELYNNVLTFGYKIARNEDVNNSLFCHS ANVNVTLLKGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQFFTQIVGNRCNEPHLPPK WVQRSSSSATAAQIKQLTEPVTNKQFLHKLNINSSSFFPYSKILPSSSSIKKLTDLR EAIFPTNLVKIPQRLKVRINLTLQKLLKRHKRLNYVSILNSICPPLEGTVLDLSHLSR OSPKERVLKFIIVILQKLLPQEMFGSKKNKGKIIKNLNLLLSLPLNGYLPFDSLLKKL RLKDFRWLFISDIWFTKHNFENLNQLAICFISWLFRQLIPKIIQTFFYCTEISSTVTI VYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLSNFNHSKMRIIPKKSNNEFR IIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKE FKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFN TNTGVLKLFNVVNASRVPKPYELYIDNVRTVHLSNQDVINVVEMEIFKTALWVEDKCY IREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPSQDTLILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKANRDKILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMN NFHIRSKSSKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSAF KDLSINVTQNMQFHSFLQRIIEMTVSGCPITKCDPLIEYEVRFTILNGFLESLSSNTS KFKDNIILLRKEIQHLQAYIYIYIHIVN

Oxytricha Euplotes LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT

·	· · · · · · · · · · · · · · · · · · ·
	Motif 0
human	AKPLHWLMSVYVVELLRSPFYVTETTFQKNR
tez1	18E1EWLVLGKRENAXHCLEDFEKRKQ1FAEF1YWLYNSF11P1LQSFFY1TESSDLRNR
EST2	LKDFRWLFISDIWFTKHNFENLNQLAICFISWLPRQLIPKIIQTFFYCTEISSTVT-
p123	TREISHMOVET-SAKHFYYFDHEN-IYVLWKLLRWIFEDLVVSLIRCFFYVTEQQKSYSK
•	. *
	Motif 1
human	LFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLRFIPKPDGL
te21	TVYFRKDIWKLLCRPYI-TSHKHEAFEKINENNVRHDTQK-TTLPPAVIRLLPKKBTP
EST2	IVYFRHDTWHKLITPFIVEYFKTYLVENNVCRNHNSYTL8NFNHSKHRIIPKKSHNEF
p123	TYYYRKNIHDVIHKHSI-ADLKKETLAEVQEKEVEEWKKS-LGFAPGKLRLIPKKTTF
22	
	Kotif 2
human	RPIVNHDYVVGARTFRREKRAERLTSRVKALP-SVLNYERA
tez1	RLITH-LRKRFLIKHGSHKKMLV6THQTLRPVASILKHLINEESSGIPFHLEVYHKLLTF
EST2	RIIAIPCRGADEEEFTIYKENHKWAIQPTQKILEYLRHKRPTSFTKIYSPTQIADRIKEF
p123	RPIMTFHKKIVNSDRKTTKLTTHTKLLHSHLMLKTLKH-RHFKDPPGPAVFHYDDVMKKY
1/22	* *
e min	
ezh	Hotif 3 (A)
tezl	KKDLLKHRHFGR-KKYFVRIDIKSCYDRIKQDLHFRIVKK-KLKDPEPVIRKYATIHATS
E872	RORLLKKFNNVLPELYFMKFDVK6CYDSIPRMECMRILKD-ALKNENGFFVRSQYFFNTN
p123	REFUCKHKQUGQPKLFFATHDIEKCYDSUNREKLSTFLKTTKLLSSDFWIHTAQILKRKW

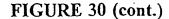
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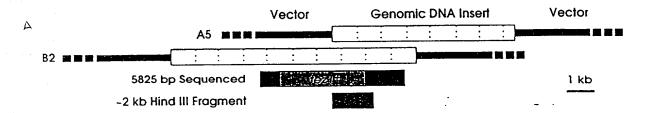
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	EST2 pep	FFYCTEISST	VTIVYFRHDT	WNKLIT	PFIVE	YFK-TYLVEN	40
	Euplotes pep	FFYVTEQQKS	YSKTYYYRKN	IWDVI-MKMS	IADLKK	ETLAEVQE	43
	Trans of tetrahymen	KHKE	GŞQIFYYRKP	IWKLVSKLTI	VKVRIQFSEK	NKOMKNNFYO	44
1	Consensus	FFY.TEK.	.ŜYYYRK,	IWKL	FK	v	50
	EST2 pep			TLSNENHSKM			79
	Euplotes pep					FREIMTFNKK	78
	Trans of tetrahymen	KIQLEEENLE	KVEEKLIPED	SFOKYPOCK	PUTPKKGS	FRHIMTFLRK	92
1	Consensus	KE		FGK	murekk	ERHIMTF . RK	100
feet							
	EST2 pep					PTQIADRIKE	129
				нтигкціки-			120
623	Trans of tetrahymen	DKOKNIK	LNLNQILMDS	OLVFRNIKO-		-QXIGYSVFD	130
100 S	Consensus	кк	LN.NLS	QL.LEKÑ-		IGVF.	150
Same of the same				D-01			
	EST2 pep			PERYFMKFD			157
				CHARTE FAIMD			155
- E. S. S.	Trans of tetrahymen	NK-QISHKFA	QF1EKWKNKG	HELENYVILL-			158
86 1 ⁶⁻² 5	Consensus	.KKE.	.FKWKG	E.EXF.T.D	CYD		186

S-1: FFY VTE TTF QKN RLF FYR KSV WSK S-2: RQH LKR VQL RDV SEA EVR QHR EA S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV

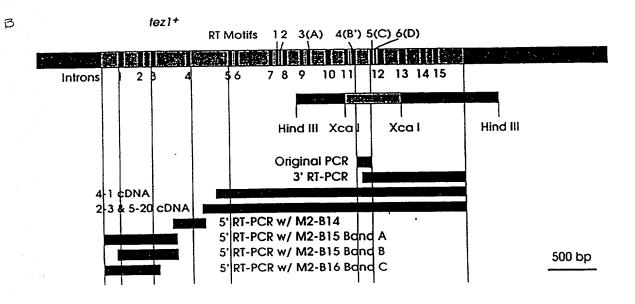


Harry Harry

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F.



Poly 4

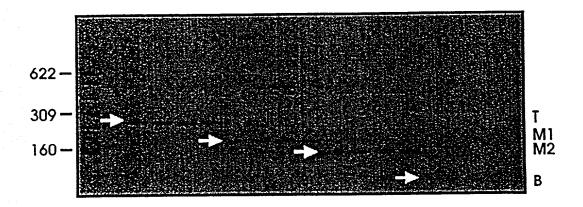
t t c t c t a a g c c t c g 5'- cag acc aaa gga att cca taa gg -3' Q T K G I P Q G

4 (B')

5 (c')

D D Y L I T

3'- ctg ctg atg gag gag tag tgg -5'
a a a a a a a a
t t t t
c c
Poly 1



Motif B' (4) QTKGIP<u>QG</u>

Motif C (5)
DDYLLIT

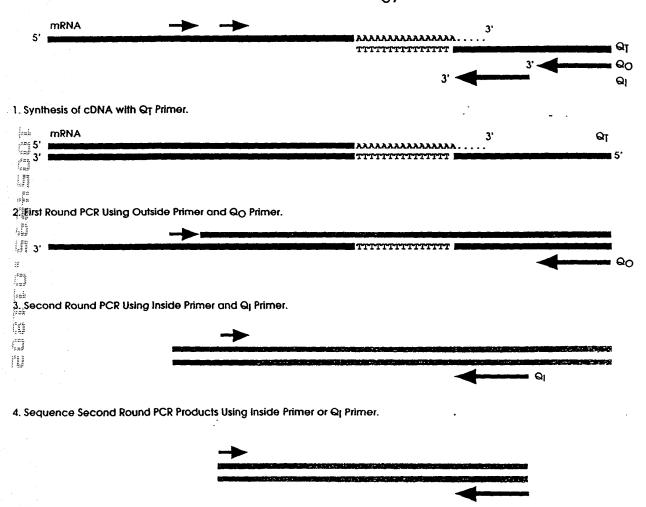
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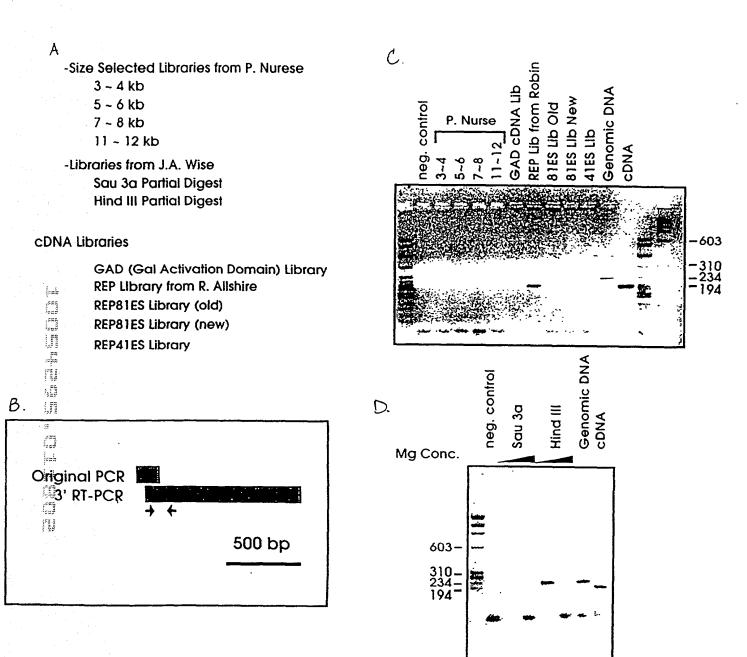
PCR Product M2 showed Reasonable Match with Other Telomerase Proteins

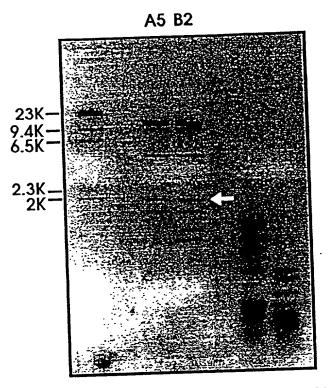
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Ot
             KGIPQGLCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
Ea_p123
                    SILSSFLCHFYMEDLIDEYLSFTKKK-----GSVLLRVV
Sp_M2
             DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS-----QDTLILKLADDFLIIS
Sc_p103
       V
         G I
caa aaa gtt ggt atc cct cag gg..... <---Actual Genomic Sequence.
            t
     t
           c c tcg
    a g
cag acc aaa gga att cca taa gg ---->
 ag acc aaa gga att cca tca ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG
 teltgg ttt cct taa ggt agt ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC
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       K G I P
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  1,13
GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT
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    D L I
              D
GTA GTC gac gac tac ctc ctc atc acc
CAT CAG ctg ctg atg gag gag tag tgg
    V D D
             Y L L
                         Ι
  <---- ctg ctg atg gag gag tag tgg
         a a aaaaa
                    t
                       t
                           t
                             t
                    c c
                           Poly 1
   .....gac gat ttc ctc ttt ata aca...... <---Actual Genomic Sequence.
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D D F L F I T

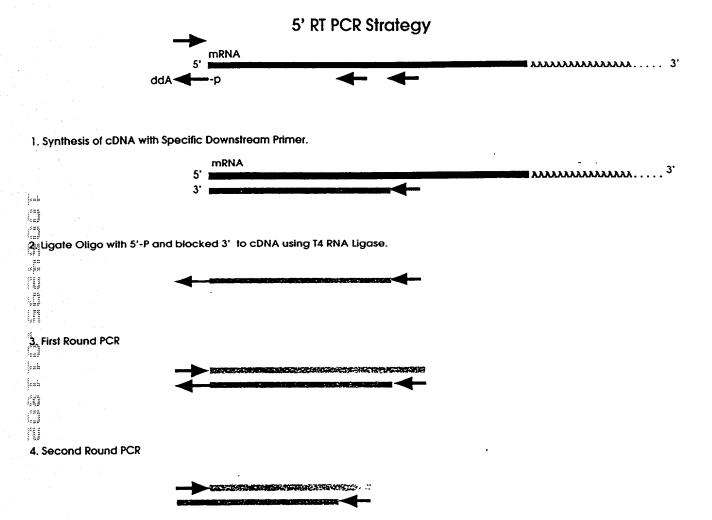
3' RT PCR Strategy







Hind III Digested Positive Genomic Clones

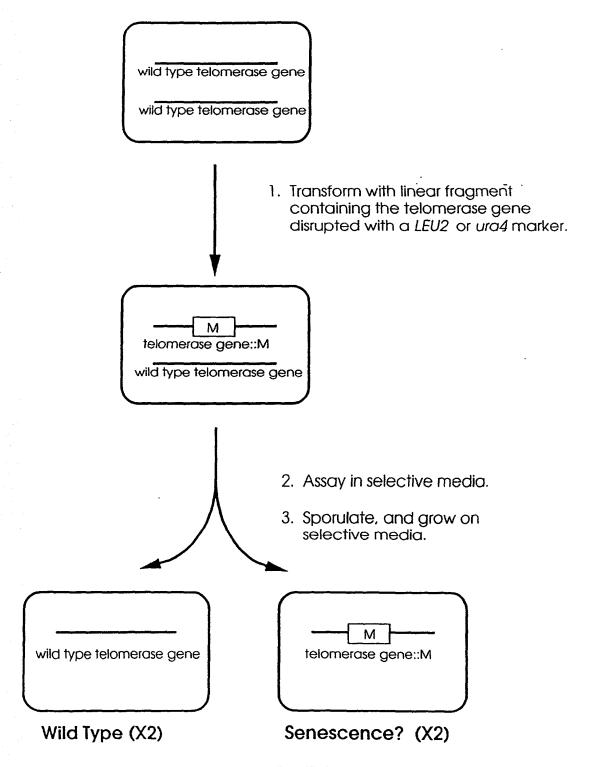


Alignment of RT Domains from Telomerase Catalytic Subunits.

```
Motif 0
  S.p. Tezlp (429). WLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIW ...(35)...
  S.c. Est2p (366). WLFRQLIPKIIQTFFYCTEISSTVT-IVYFRHDTW ...(35)...
  E.a. p123 (441). WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIW ...(35)...
               Motif 1
                           Motif 2
              p hh h K
                          hR h
                                       R
              AVIRLLPKK--NTFRLITN-LRKRF ... (61)...
  S.p. Tezlp
              SKMRIIPKKSNNEFRIIAIPCRGAD ...(62)...
  S.c. Est2p
              GKLRLIPKK--TTFRPIMTFNKKIV ... (61)...
⊭ E.a. p123
              Motif 3(A) AF
                  h hDh GY
                             h
               KKYFVRIDIKSCYDRIKQDLMFRIVK ...(89)...
  S.p. Tezlp
              ELYFMKFDVKSCYDSIPRMECMRILK ... (75)...
  S.c. Est2p
               KLFFATMDIEKCYDSVNREKLSTFLK ... (107)...
  E.a. p123
                       ***
E CHOO
                Motif 4(B')
                     hPQG
                            pP hh
                                    h
               YLOKVGIPQGSILSSFLCHFYMEDLIDEYLSF ...(6)...
  S.p. Tezlp
               YIREDGLFQGSSLSAPIVDLVYDDLLEFYSEF ...(8)...
  S.c. Est2p
               YKOTKGIPOGLCVSSILSSFYYATLEESSLGF ... (14) ...
  E.a. p123
                                                 Motif 6(D)
                   Y Motif 5(C)
See and
                                                 Gh h cK h
                t. F DDhhh
               VLLRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENS . (205)
  S.p. Tezlp
               LILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKANRDKILAVSSQS .(173)
   S.c. Est2p
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   E.a. p123
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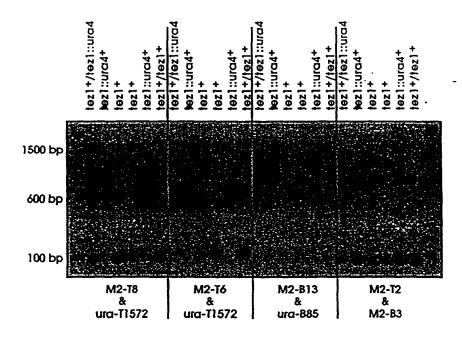
SO, TOD ... LENGTH STATE THE THE TOTAL THE TANK TO THE TANK THE TA So_Total 70 KKQ ------SY TV VV --- F VNKKDEKK 76
Sc_Endo on SP GO -----TE I KK A SE I SE DOOOY IN on
En 123 D EE MAP EN PRIVING A TE YELL GERNAVE. Sp. Tip1p see LHRREAM -Sc. Est2p att I Y I HE Y H -Es n123 see OSL I OYEA

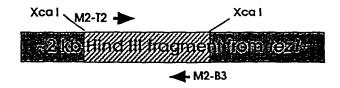
Disruption strategy for the putative telomerase genes.

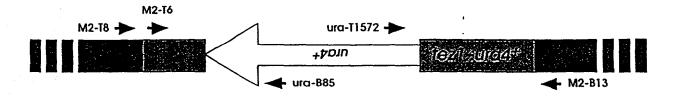


(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

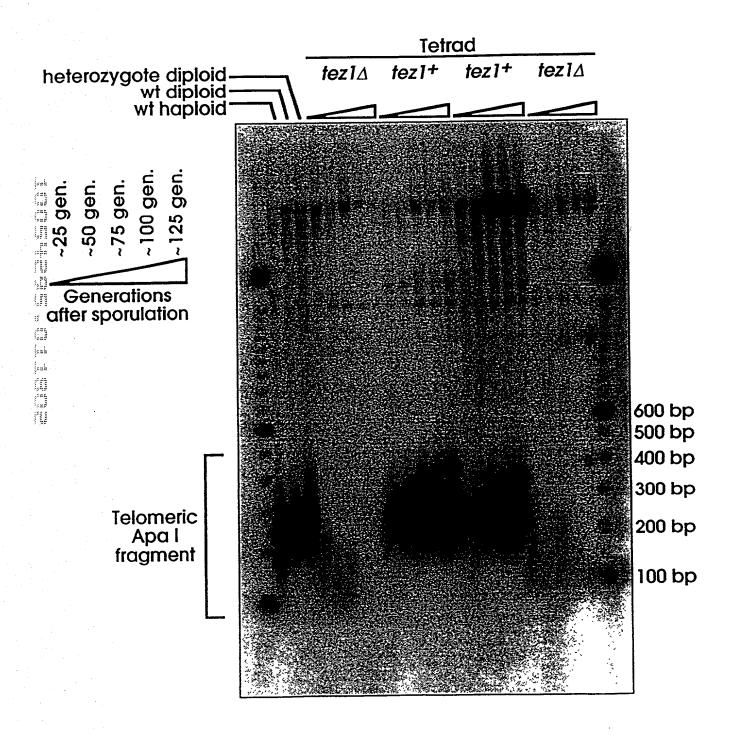
An Example of Confirmation of tez1 disruption By PCR







Tez1 disruption causes progressive shortening of telomeres in S. pombe



1 ggtacco			- +				rt a a i	++~~1	-+	cas	acac	toot	aaat,	-t-ct	a s n r	atat		2022	72 80	
81 actca	•					_		_		_	-							-	-	60
161 ccaaq	•			_						-									_	
241 ggtto	-			_		-		-			-						_			
321 agcto																				
401 ttaac			-		-		_									-	-	_	_	
481 gttga	itaai	ttati	ttgca	aaaa	tcate	gtcc	ttag	tggtg	ggta	atcc	gcga	aagt	tttt	tgate	gctt	gcac	acgt	ctago	catg	560
561 attga	ıgata	attca	aaaaa	attt	ctato	ccaci	tacaa	actco	cttta	aacg	cggt	ttta	tttt	tctat	tttt	ctat	tctc	atgtt	tgtt	640
641 ccaaa	itate	gtate	catc	cgta	attag	gcti	tttt	tccgt	tttt	actc	ctgg	aatc	gtac	cttt	ttca	ctat	tccc	cctaa	atga	720
721 ataat	cta	aatta	agtt	cgct	tata	aatt	gata	gtagt	tagaa	aaga	ttgg	tgat	tcta	ctcgi	tgta	atgti	tatt	agtt	taaa	800
801 gata	ttt	gcaaa	acat	ttai	tage	ctate	catta	atata	aaaa	aaaa	tcct	ataa	ttata	aaata	atta	atca	atat	ttgcg	ggtc	880
881 actat	tta	tttaa	aaac	gttai	tgato	cagta	agga	cact	ttgca	atat	atat	agtt	atgc	ttaa	tggt	tact	tgta	actto	gc	958
959 ATG 2	CC (GAA (CAC	CAT A	ACC (CCC I	AAA	AGC Z	AGG A	ATT	CTT	CGC	TTT (CTA (GAG .	AAT (CAA !	TAT (STA	1018
1 M = 5	. 1	E I	- I	4 C	r I	P 1	к :	S I	R :	Ι :	L	R	F :	L 1	Ε	N (Ω.	Y 1	J .	20
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. ,	CTA	TGT	ACC	TTA	AAT	GAT	TAT	GTA	CAA	CTT	GTT	TTG	AGA	GGG	TCG	CCG	GCA	AGC	TCG	1078
21 Y	L	С	T	L,	N	D	Y	ν	Q	L	V	L	R	G	S	P	A	S	s	40
765 A									-											
1079 TAT	AGC	AAT	АТА	TGC	GAA	CGC	TTG	AGA	AGC	GAT	GTA	CAA	ACG	ጥርር	ተተ	ጥርጥ	ስጥጥ	TTT	CTT	1138
41 ¥	S	N																		-
			I	С	E	R	L	R	s	D	V		т	s	F	s	I		L	60
(Fig.)	. •	14	1	С	E	R	L	R	s			Q						F	L	60
1139 CAT			_							D	V	Q	T	s	F	s	I	F		
18	TCG	ACT	GTA	GTC	GGC	TTC	GAC	AGT	AAG	D CCA	V GAT	Q GAA	T GGT	s GTT	F CAA	s TTT	I TCT	F TCT	CCA	1198
61 <u>≈</u> #			_							D	V	Q	T	s	F	s	I	F		
61.≅#I	TCG	ACT	GTA	GTC	GGC	TTC	GAC	AGT	AAG	D CCA	V GAT	Q GAA	T GGT	s GTT	F CAA	s TTT	I TCT	F TCT	CCA	1198
61:2H	TCG	ACT	GTA	GTC	GGC	TTC	GAC	AGT	AAG	D CCA	V GAT	Q GAA	T GGT	s GTT	F CAA	s TTT	I TCT	F TCT	CCA	1198
61 carried	TCG	ACT	GTA	GTC	GGC	TTC	GAC	AGT	AAG	D CCA	V GAT	Q GAA	T GGT	s GTT	F CAA	s TTT	I TCT	F TCT	CCA	1198
61 carried	TCG	ACT	GTA	GTC	GGC	TTC	GAC	AGT	AAG	D CCA	V GAT	Q GAA	T GGT	s GTT	F CAA	s TTT	I TCT	F TCT	CCA	1198
61:2H	TCG	ACT	GTA	GTC	GGC	TTC	GAC	AGT	AAG	D CCA	V GAT	Q GAA	T GGT	s GTT	F CAA	s TTT	I TCT	F TCT	CCA	1198

1199 81		TGC C	TCA S	CAG Q	TCA S	GAG E	gtat	atat	attt	ttgt	tttg	attt	ttt	ctat	tcgg	gata	gcta	atat	atgg	gcag	1272 86
1273 87		ATA I	GCG A	AAT N	GTT V	GTA V	AAA K	CAG Q	ATG M	TTC F	GAT D	GAA E	AGT S	TTT F	GAG E	CGT R	CGA R	agg R	AAT N	CTA L	1332 106
1333 107		atg M	AAA K	GGG G	TTT F	TCC S	atg M	gtaa	iggta	ittet	aatt	:gtga	aata	ittta	cctg	caat	tact	gttt	caaa	igaga	1405 113
1406 114	ttgt	atti	aaco	gata	aaag	AAT N	CAT H	GAA E	GAT D	TTT F	CGA R	GCC A	ATG M	CAT H	GTA V	aac N	GGA G	GTA V	CAA Q	AAT N	1469 128
1470 129		CTC L	GTT V	TCT S	ACT T	TTT F	CCT P	AAT N	TAC Y	CTT L	ATA I	TCT S	ATA I	CTT L	GAG E	TCA S	AAA K	AAT N	TGG W	CAA Q	1529 148
1530 149		TTG L	TTA L	GAA E	AT G	gtaaa	ataco	ggtt	aaga	tgtt	gcgc	cact	tgaa	acaag	acto	jacaa	agtat	ag T	ora o	G GGC	1601 155
1602 156		GAT D	GCC A	atg M	CAT H	TAC Y	TTA L	TTA L	TCC S	aaa K	GGA G	agt S	ATT I	TTT F	gag E	GCT A	CTT L	CCA P	aat N	GAC D	1661 175
1662 176	2.2	TAC Y	CTT L	CAG Q	ATT I	TCT S	GGC G	ATA I	CCA P	CTT L	TTT F	AAA K	AAT N	AAT N	GTG V	TTT F	GAG E	GAA E	ACT T	GTG V	1721 195
1722 196		AAA K	AAA K	aga R	aag K	CGA R	ACC T	ATT I	GAA E	ACA T	TCC S	ATT I	ACT T	CAA Q	aat N	aaa K	AGC S	GCC A	CGC R	AAA K	1781 215
1782 216		GTT V	TCC S	TGG W	AAT N	AGC S	ATT I	TCA S	ATT I	agt s	AGG R	TTT F	AGC S	ATT I	TTT F	TAC Y	AGG R	TCA S	TCC S	TAT Y	1841 235
1842	ĀAG	AAG	TTT	AAG	CAA	G gt	taac	aata	actgt	tato	cctto	cata	actaa	attti	tag 1	AT C	ra T	AT T	KA TT	AC	
1907 236		K	F	ĸ	Q	D										L	Y	F	N		245
1908 246		CAC H	TCT	ATT I	TGT C	GAT D	CGG R	AAC N	ACA T	GTA V	CAC H	ATG M	TGG W	CTT L	CAA Q	TGG W	ATT I	TTT F	CCA P	AGG R	1967 265
1968 266	CAA Q			CTT L	ATA I		GCA A			gtg V		CAA Q		CAC H	AAA K	g t g V	ATT I	CCA P	CTG L	GTA V	2027 285
2028 286		CAG Q		ACA T	GTT V	GTG V	CCC P	AAA K	CGT R	CTC L		aag K	GTA V	TAC Y	CCT P	TTA L	ATT I	GAA E	CAA Q	ACA T	2087 305
2088 306		AAG K	CGA R	CTC L	CAT H	CGT R	ATT I		CTA L	TCA S		GTT V	TAC Y	AAC N	CAT H	TAT Y	TGC C	CCA P	TAT Y	ATT I	2147 325
2148 326		ACC T	CAC H	GAT D	GAT D	GAA E	AAA K	ATC I	CTT L	AGT S	TAT Y	TCC S	TTA L	aag K	CCG P	AAC N	CAG Q	GTG V	TTT F	GCG A	2207 345
2208 346		CTT L		TCC S		CTT L	GTT V	CGA R	GTG V	TTT F	CCT P	AAA K	TTA L	ATC I	TGG W	GGT G	AAC N	CAA Q	AGG R	ATA I	2267 365
	TTT F					AAA K	G g	tatt	gtata	aaaal	tttai	ttac	cacta	aacg.	attt	tacc	ag A	C CT	C GA. E	A ACT	2336 375

2337 376		TTG L	aaa K	TTA L	TCG S	AGA R	TAC Y	gag E	TCT S	TTT F	AGT S	TTA L	CAT H	TAT Y	TTA L	atg M	AGT S	AAC N	ATA I	AAG K	2396 395
2397 396	gta	atat	gcca	aatt	tttt	tacc	atta	atta	acaa	tcag	ATT I	TCA S	gaa E	TTA I	GAA E	TGG W	CTA L	GTC V	CTT L	GGA G	2465 405
2466 406		AGG R	TCA S	AAT N	GCG A	AAA K	ATG M	TGC C	TTA L	AGT S	GAT D	TTT F	GAG E	AAA K	CGC R	aag K	CAA Q	ATA I	TTT F	GCG A	2525 425
2526 426		TTC F	ATC I	TAC Y	TGG W	CTA L	TAC Y	AAT N	TCG S	TTT F	ATA I	ATA I	CCT P	ATT I	TTA L	CAA Q	TCT S	TTT F	TTT F	TAT Y	2585 445
2586 446		ACT T	GAA E	TCA S	AGT S	GAT D	TTA L	CGA R	AAT N	CGA R	ACT T	GTT V	TAT Y	TTT F	AGA R	AAA K	GAT D	ATT I	TGG W	AAA K	2645 465
2646 466		TTG L	TGC C	CGA R	CCC P	TTT F	ATT I	ACA T	TCA S	atg M	AAA K	ATG M	GAA E	GCG A	TTT F	gaa E	AAA K	-ATA I	AAC N	GAG E	2705 485
7. 4	gta	ttt	aaag	tatt	tttt	gcaaa	aaago	ctaa	tatti	tca	AA E N	N C	r GT? V	r ago	M E	G GAT	r act	CAC Q	G AAA K	A ACT T	2775 495
2776 496	ACT T	TTG L	CCT P	CCA P	GCA A	GTT V	ATT I	CGT R	CTA L	TTA L	CCT P	AAG K	AAG K	TAA N	ACC T	TTT F	CGT R	CTC L	ATT	ACG T	2835 515
2836 516		TTA L	AGA R	AAA K	AGA R	TTC F	TTA L	ATA I	aag K	gta	ttaai	tttt	ggt	catca	aatgi	tacti	tacı	teta	aatct	atta	2906 524
2907 525			M	G	S	N	K	K	M	L	V	S	T	N	Q	T	L	R	P	v	2967 542
2968 543	A	S	I	L	K	Н	L	I	N	E	E	S	S	G	I	P	F	N	L	E	3027 562
563	V	Y	М	K	L	L .	T	F	K	K	D	L	L	K	Н	R	М	F	G	gtaat	581
3089 582			, ,							I	R I	(I	ζ !	? E	7	J I	₹]	[])]	Ţ.	3155 591
3156 592		TCC S	TGT C	TAT Y	GAT D	CGA R	ATA I	aag K	CAA Q	GAT D	TTG L	ATG M	TTT F	CGG R	ATT I	GTT V	AAA K	aag K	AAA K	CTC L	3215 611
3216 612	K	D	P	E	F	V	I	R	ĸ	Y	A	T	I	Н	A	T	S	D	R	A	3275 631
	ACA T		AAC N	TTT F	GTT V	AGT S	GAG E	GCG A	TTT F	TCC S	TAT Y	T gt	caagt	ttat	ttt	ttcai	ttgga	aatti	tttt	acaa	3343 643
3344 644					D	М	V	P	F	E	K	V	V	Q	L	L	S	M	K	Т	3405 659
3406 660	S	D	T	L	F	V	D	F	V	D	Y	W	T	K	s	S	S	E	I	F	3465 679
3466 680		ATG M	CTC L	AAG K	GAA E	CAT H	CTC L	TCT S	GGA G	CAC H	ATT I	GTT V	aag K	gtat	acca	aatt	gttga	aatto	gtaat	aaca	3532 692

3533 693	cta	atga	aact	ag A' I		GA A	AT T(CT CA Q	AA TA Y	AC C' L	PT CA Q	AA AA	AA G1	TT G(G	GT A	rc co	CT CA Q	AG GC	GC TC S	CA	3593 708
3594 709		CTG L	TCA S	TCT S	TTT F	TTG L	TGT C	CAT H	TTC F	TAT Y	ATG M	GAA E	GAT D	TTG L	ATT I	GAT D	GAA E	TAC Y	CTA L	TCG S	3653 728
365 4 729		ACG T	AAA K	AAG K	AAA K	GGA G	TCA S	GTG V	TTG L	TTA L	CGA R	GTA V	GTC V	GAC D	GAT D	TTC F	CTC L	TTT F	ATA I	ACA T	3713 748
3714 749		aat N	aaa K	aag K	GAT D	GCA A	aaa K	aaa K	TTT F	TTG L	aat N	TTA L	TCT S	TTA L	aga R	G gi	gagt	tgct	gtca	attcc	3777 764
3778 765	taa	gttc	taac	cgtt	gaag						TAA							AAA A			3840 778
3841 779	I	AAC N		GAA E	AAT N	AGT S	AAT N	GGG G	ATA I	ATA I	AAC N	AAT N	ACT T	TTT F	TTT F	AAT N	GAA E	AGC S	aag K	AAA K	3900 798
3901=			CCA P	TTC F	TTC F	GGT G	TTC F	TCT S	GTG V	AAC N	ATG M	AGG R	TCT S	CTT L	GAT D	ACA T	TTG L	TTA L	GCA A	TGT C	3960 818
3961 819		AAA K	ATT I	GAT D	GAA E	GCC A	TTA L	TTT F	aac N	TCT S	ACA T	TCT S	gta V	gag E	CTG L	ACG T	AAA K	CAT H	atg M	GGG G	4020 838
4021 839	7	TCT S	TTT F	TTT F	TAC Y	AAA K	ATT I	CTA L	AG (gtata	actg	tgtaa	actga	aataa	atago	ctgad	caaat	aato	cag A	Y TCG S	4089 848
4090 849	s	CTT L	GCA A	TCC S	TTT F	GCA A	CAA Q	GTA V	TTT F	ATT I	GAC D	ATT I	ACC T	CAC H	AAT N	TCA S	AAA K	TTC F	AAT N	TCT S	4149 868
4150 869	С	С	N	I	Y	R	L	G	Y	S	M	С	M	R	A	Q	A	Y	TTA L	K	4209 888
889	R	M	К	D	I	F		P	Q	R	M	F	I	T	D					taga	903
904	•					-	L	L	N	V	I	G	R	K	I	W	K	ĸ	L	A A	917
918	E	I	L	G	Y	Т	s	R	R	F	L	S	S	A	E	V	K	W		gtgtc	935
936						•			_	L	F	С	L	G	М	R	D	G	L	K	4468 946
947	P	S	F	K	Y	Н	P	С	F	Е	Q	L	I	Y	Q	F	Q	S	L	T	4528 966
	D	L	I	K	P	L	R	P	V	L	R	Q	V	L	F	L	Н	R	R	I	4588 986
4589 987		GAT D	TAA *	tgtc	attt	tcaa	ttta	ttat	atad	catco	ttta	attad	tggt	gtc	ttaa	acaa	catta	attac	taag	tata	4665 989

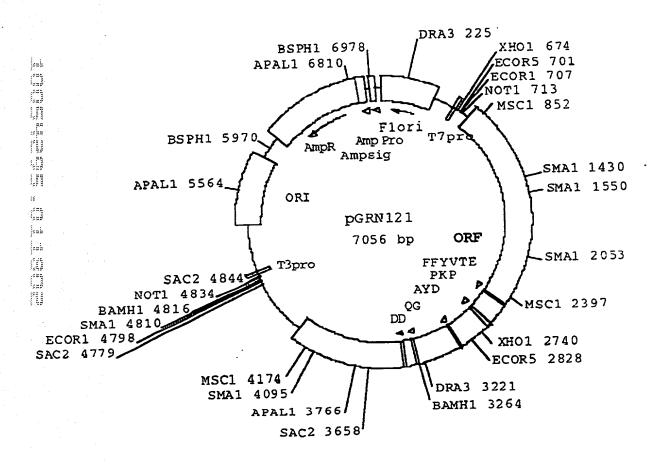
1666	gctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctcgttattagttttgattga	4745
1746	$\verb ttatccttatacttttaagaaagattgacagtggttgctgactactgcccacatgcccattaaacgggagtggttaaaca $	4825
1826	ttaaaagtaatacatgaggctaatctcctttcatttagaataaggaaagtggttttctataatgaataatgcccgcacta	4905
1906	atgcaaaaagacgaagattatcttctaaacaagggggattaagcatatccgaaggaaaagagagtaatatacccagtgtt	4985
4986	$\tt gttgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaaattttggtgaccgaattttggtaaaagc$	5065
5066	$\verb cccaggttatccatggtggccggccttgctactgagacgaaaagaaactaaggatagtttgaatactaatagctcattta \\$	5145
	$\verb atgtcttatataaaggttttgtttttcctgacttcaattttgcatgggtgaaaagaaatagtgttaagccattattggat $	
	tccgaaatagccaaatttcttggttcctcaaagcggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcc	
	${\tt tcctgatttaaaggaggaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaatttttgc}$	
	aaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcggagagtatctccagcggatccttgatgtcaata	
	acttctatttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctctacgcagttaagtgaccaaaggtacc	

GCC	AAGTT	rccto	GCACT	rggci	:G	1 met ATG	ser AGT	val GTG	tyr TAC	val GTC	val GTC	glu GAG	leu CTG	leu CTC
10 arg AGG	ser TCT	phe TTC	phe TTT	tyr TAT	val GTC	thr ACG	glu GAG	thr ACC	thr ACG	20 phe TTT	gln CAA	lys AAG	asn AAC	arg AGG
leu CTC	phe TTT	phe TTC	tyr TAC	arg CGG	30 lys AAG	ser AGT	val GTC	trp TGG	ser AGC	lys AAG	leu TTG	gln CAA	ser AGC	ile ATT
40 gly GGA	ile ATC	arg AGA	gln CAG	his CAC	leu TTG	lys AAG	arg AGG	val GTG	gln CAG	50 leu CTG	arg CGG	glu GAG	leu CTG	ser TCG
glu GAA	ala GCA	glu GAG	val GTC	arg AGG	60 gln CAG	his CAT	arg CGG	glu GAA	ala GCC	arg AGG	pro CCC	ala GCC	leu CTG	leu CTG
70 thr ACC	ser TCC	arg AGA	leu CTC	arg CGC	phe TTC	ile ATC	pro CCC	lys AAG	pro CCT	80 asp GAC	gly GGG	leu CTG	arg CGG	pro CCG
ile ATT	val GTG	asn AAC	met ATG	asp GAC	90 tyr TAC	val GTC	val GTG	gly GGA	ala GCC	arg AGA	thr ACG	phe TTC	arg CGC	arg AGA
100 glu GA	lys A AAG	ARG	ala GCC	glu GAG	arg CGT	leu CTC	thr ACC	ser TCG	arg AGG	110 val GTG	lys AAG	ala GCA	leu CTG	phe TTC
sei AG0	val	leu CTC	asn AAC	tyr	120 glu GAG	arg CGG	ala GCG	arg CGG	arg CGC	pro CCC	gly GGC	leu CTC	leu CTG	gly GGC
130 ala GC0	ser	val GTG	leu CTG	gly GGC	leu CTG	asp GAC	asp GAT	ile ATC	his CAC	140 arg AGG	ala	trp TGG	arg CGC	thr ACC
phe TT(e val C GTG	leu CTG	arg CGT	val GTG	150 arg CGG	ala GCC	gln CAG	asp GAC	pro CCG	pro CCG	pro CCT	glu GAG	leu CTG	tyr TAC
160 phe TT	val	lys AAG	val GTG	asp GAT	val GTG	thr ACG	gly GGC	ala GCG	tyr TAC	170 asp GAC	thr	ile ATC	pro CCC	gln CAG
ası GA(o arg	leu CTC	thr ACG	glu GAG	180 val GTC	ile ATC	ala GCC	ser AGC	ile ATC	ile ATC	lys	pro	gln CAG	asn AAC

190 thr ACG	tyr TAC	cys TGC	val GTG	arg CGT	arg CGG	tyr TAT	ala GCC	val GTG	val GTC	200 gln CAG	lys AAG	ala GCC	ala GCC	met ATG
gly GGC	thr ACG	ser TCC	ala GCA	arg AGG	210 pro CCT	ser TCA	arg AGA	ala GCC	thr ACG	ser TCC	tyr TAC	val GTC	gln CAG	cys TGC
220 gln CAG	gly GGG	ile ATC	pro CCG	gln CAG	ggc gly	ser TCC	ile ATC	leu CTC	ser TCC	230 thr ACG	leu CTG	leu CTC	cys TGC	ser AGC
leu CTG	cys TGC	tyr TAC	gly GGC	asp GAC	240 met ATG	glu GAG	asn AAC	lys AAG	leu CTG	phe TTT	ala GCG	gly GGG	ile ATT	arg CGG
250 arg CGG	asp GAC	gly GGG	leu CTG	leu CTC	leu CTG	arg CGT	leu TTG	val GTG	asp GAT	260 asp GAT	phe TTC	leu TTG	leu TTG	val GTG
thr ACA	pro CCT	his CAC	leu CTC	thr ACC	270 his CAC	ala GCG	lys AAA	thr ACC	phe TTC	leu CTC	arg AGG	thr ACC	leu CTG	val GTC
280 arg CGA	gly GGT	val GTC	pro CCT	glu GAG	tyr TAT	gly GGC	cys TGC	val GTG	val GTG	290 asn AAC	leu TTG	arg CGG	lys AAG	thr ACA
val GTG	val GTG	asn AAC	phe TTC	pro CCT	300 val GTA	glu GAA	asp GAC	glu GAG	ala GCC	leu CTG	gly GGT	gly	thr ACG	ala GCT
310 phe TTT	val GTT	gln CAG	met ATG	pro. CCG	ala GCC	his CAC	gly GGC	leu CTA	phe TTC	320 pro CCC	trp TGG	cys TGC	gly GGC	leu CTG
 leu CTG	leu CTG	asp GAT	thr ACC	arg CGG	330 thr ACC	leu CTG	glu GAG	val GTG	gln CAG	ser AGC	asp GAC	tyr TAC	ser TCC	ser AGC
340 tyr TAT	ala GCC	arg CGG	thr ACC	ser TCC	ile ATC	arg AGA	ala GCC	ser AGT	leu CTC	350 thr ACC	phe	asn AAC	arg	gly
phe TTC	lys AAG	ala GCT	gly GGG	arg AGG	360 asn AAC	met ATG	arg CGT	arg CGC	lys AAA	leu CTC	phe	gly	val	leu TTG
370	len	lvs	cvs	his	ser	leu	phe	leu	asp	380 leu	gln	ı val	. asn	ser AGC

	leu CTC	gln CAG	thr ACG	val GTG	cys TGC	390 thr ACC	asn AAC	ile ATC	tyr TAC	lys AAG	ile ATC	leu CTC	leu CTG	leu CTG	gln CAG
	400 ala GCG	tyr TAC	arg AGG	phe TTT	his CAC	ala GCA	cys TGT	val GTG	leu CTG	gln CAG	410 leu CTC	pro CCA	phe TTT	his CAT	gln CAG
	gln CAA	val GTT	trp TGG	lys AAG	asn AAC	420 pro CCA	his CAT	phe TTT	ser TCC	cys TGC	ala GCG	ser TCA	ser TCT	leu CTG	thr ACA
	430 arg CGG	leu CTC	pro CCT	leu CTG	leu CTA	leu CTC	his CAT	pro CCT	glu GAA	ser AGC	440 gln CAA	glu GAA	arg CGC	arg AGG	asp _GAT
The first of the f	val GTC	ala GCT	gly	gly GGC	gln CAA	450 gly GGG	arg CGC	arg CGC	arg CGG	pro CCC	ser TCT	ala GCC	leu CTC	arg CGA	gly GGC
Steers Hally and Daniel	460 arg CGT	ala GCA	val GTG	ala GCT	val GTG	pro CCA	pro CCA	ser AGC	ile ATT	pro CCT	470 ala GCT	gln CAA	ala GCT	asp GAC	ser TCG
H. H	thr ACA	pro CCG	cys TGT	his CAC	leu CTA	480 arg CGT	ala GCC	thr ACT	pro CCT	gly GGG	val GTC	thr ACT	gln CAG	asp GAC	ser AGC
the property of	490 pro CCA	asp GAC	ala GCA	ala GCT	glu GAG	ser TCG	glu GAA	ala GCT	pro CCC	gly GGG	500 asp GAC	asp GAC	ala GCT	asp GAC	cys TGC
***	pro CCT	gly GGA	gly GGC	arg CGC	ser AGC	510 gln CAA	pro CCC	gly GGC	thr ACT	ala GCC	leu CTC	arg AGA	leu CTT	gln CAA	asp GAC
	520 his CAT	pro	gly GGA	leu CTG	met ATG	ala GCC	thr ACC	arg CGC	pro CCA	gln CAG	530 pro CCA	gly	arg CGA	glu GAG	gln CAG
	thr ACA	pro CCA	ala GCA	ala GCC	leu CTG	540 ser TCA	arg CGC	arg CGG	ala GCT	tyr TAT	thr ACG	ser TCC	gln CAG	gly GGA	gly GGG
	550 arg AGG	gly GGC	gly GGC	pro CCA	his CAC	pro CCA	gly GGC	leu CTG	his CAC	arg CGC	560 trp TGG	glu GAG	ser TCT	glu GAG	ala GCC
	564 OP TGA	GTG.	AGTG	TTTG	GCCG.	AGGC	CTGC.	ATGT	ccgg	CTGA	AGGC	TGAG	TGTC	CGGC	TGAGGC
	CTG.	AGCG.	AGTG	TCCA	GCCA	AGGG	CTGA	GTGT	CCAG	CACA	.CCTG	CGTT	TTCA	CTTC	CCCAC

	Motif -1 Ep p123 Sp Tez1 Sc Est2 Hs TCP1 consensus	LVVSLIRCFFYVTEQQKSYSKTFIIPILQSFFYITESSDLRNRTLIPKIIQTFFYCTEISSTVTIVYVVELLRSFFYVTETTFQKNRL FFY TE
•	Motif 0 Ep p123 Sp Tez1 Sc Est2 Hs TCP1 consensus	K phhh K hR h RKSLGFAPGKLRLIPKKTTFRPIMTFNKKIVQKTTLPPAVIRLLPKKNTFRLITNLRKRFLTLSNFNHSKMRIIPKKSNNEFRIIAIPCRGADARPALLTSRLRFIPKPDGLRPIVNMDYVVG. R PK R I
or 18 1 made Very Walt gr	Motif A Ep p123 Sp Tez1 Sc Est2 Hs TCP1 consensus	AF h hDh GY hPKLFFATMDIEKCYDSVNREKLSTFLKRKKYFVRIDIKSCYDRIKQDLMFRIVKPELYFMKFDVKSCYDSIPRMECMRILKPELYFVKVDVTGAYDTIPQDRLTEVIA// F D YD
Mr. Mr. Gardt and Targe Tax	Motif B Ep p123 Sp Tez1 Sc Est2 Hs TCP1 consensus	hPQG pS hhNGKFYKQTKGIPQGLCVSSILSSFYYAGNSQYLQKVGIPQGSILSSFLCHFYMEEDKCYIREDGLFQGSSLSAPIVDLVYDRATSYVQCQGIPQGSILSTLLCSLCYG G QG S
March Grand Charle	Motif C Ep p123	Y h F DDhhh PNVNLLMRLTDDYLLITTQENN
	Sp Tez1 Sc Est2 Hs TCP1 consensus	KKGSVLLRVVDDFLFITVNKKD SQDTLILKLADDFLIISTDQQQ RRDGLLLRLVDDFLLVTPHLTH DD L
	Motif D Ep p123 Sp Tezl Sc Est2 Hs TCP1 consensus	Gh h cKNVSRENGFKFNMKKLLNLSLRGFEKHNFSTKKLAMGGFQKYNAKALRTLVRGVPEYGCVV G



1 GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC

51 CCGCGATGCC GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC 101 AGCCACTACC GCGAGGTGCT GCCGCTGGCC ACGTTCGTGC GGCGCCTGGG 151 GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG GGACCCGGCG GCTTTCCGCG 201 CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN ANGGCNGCCC 251 CCCGCCGCCCCTCCTTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC 301 CCGAGTGCTG CANANGCTGT GCGANCGCGG CGCGAANAAC GTGCTGGCCT 351 TCGGCTTCGC GCTGCTGGAC GGGGCCCGCG GGGGCCCCCC CGAGGCCTTC 401 ACCACCAGCG TGCGCAGCTA CCTGCCCAAC ACGGTGACCG ACGCACTGCG 451 GGGGAGCGG GCGTGGGGGC TGCTGCTGCG CCGCGTGGGC GACGACGTGC 501 TGGTTCACCT GCTGGCACGC TGCGCGNTNT TTGTGCTGGT GGNTCCCAGC 551 TGCGCCTACC ANGTGTGCGG GCCGCCGCTG TACCAGCTCG GCGCTGCNAC 601 TCAGGCCGG CCCCGCCAC ACGCTANTGG ACCCGAANGC GTCTGGGATC 651 CAACGGCCT GGAACCATAG CGTCAGGGAG GCCGGGGTCC CCCTGGGCTG 701 CCAGCCCGG GTGCGAGGAG GCGCGGGGC AGTGCCAGCC GAAGTCTGCC 751 GTTGCCCAAG AGGCCCAGGC GTGGCGCTGC CCCTGAGCCG GAGCGGACGC 801 CCGTTGGGCA GGGGTCCTGG GCCCACCCGG GCAGGACGCC TGGACCGAGT 851 GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC 901 CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCCAC CCATCCGTGG 951 GCCGCCAGCA CCACGCGGGC CCCCCATCCA CATCGCGGCC ACCACGTCCT 1001 GGGACACGCC TTGTCCCCCG GTGTACGCCG AGACCAAGCA CTTCCTCTAC 1051 TCCTCAGGCG ACAAGNACAC TGCGNCCCTC CTTCCTACTC AATATATCTG 1101 AGGCCCAGCC TGACTGGCGT TCGGGAGGTT CGTGGAGACA NTCTTTCTGG 1151 TTCCAGGCCT TGGATGCCAG GATTCCCCGC AGGTTGCCCC GCCTGCCCCA 1201 GCGNTACTGG CAAATGCGGC CCCTGTTTCT GGAGCTGCTT GGGAACCACG 1251 CGCAGTGCCC CTACGGGGTG TTCCTCAAGA CGCACTGCCC GCTGCGAGCT 1301 GCGGTCACCC CAGCAGCCGG TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC 1351 TGTGGCGGCC CCCGAGGAGG AGGAACACAG ACCCCCGTCG CCTGGTGCAG 1401 CTGCTCCGCC AGCACAGCAG CCCCTGGCAG GTGTACGGCT TCGTGCGGGC 1451 CTGCCTGCGC CGGCTGGTGC CCCCAGGCCT CTGGGGCTCC AGGCACAACG 1501 AACGCCGCTT CCTCAGGAAC ACCAAGAAGT TCATCTCCCT GGGGAAGCAT 1551 GCCAAGCTCT CGCTGCAGGA GCTGACGTGG AAGATGAGCG TGCGGGACTG 1601 CGCTTGGCTG CGCAGGAGCC CAGGGGTTGG CTGTGTTCCG GCCGCAGAGC 1651 ACCGTCTGCG TGAGGAGATC CTGGCCAAGT TCCTGCACTG GCTGATGAGT 1701 GTGTACGTCG TCGAGCTGCT CAGGTCTTTC TTTTATGTCA CGGAGACCAC 1751 GTTTCAAAAG AACAGGCTCT TTTTCTACCG GAAGAGTGTC TGGAGCAAGT 1801 TGCAAAGCAT TGGAATCAGA CAGCACTTGA AGAGGGTGCA GCTGCGGGAG 1851 CTGTCGGAAG CAGAGGTCAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT 1901 GACGTCCAGA CTCCGCTTCA TCCCCAAGCC TGACGGGCTG CGGCCGATTG 1951 TGAACATGGA CTACGTCGTG GGAGCCAGAA CGTTCCGCAG AGAAAAGAGG 2001 GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTCAGCG TGCTCAACTA 2051 CGAGCGGCG CGCCCCCG GCCTCCTGGG CGCCTCTGTG CTGGGCCTGG 2101 ACGATATCCA CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCCCAG 2151 GACCGCCGC CTGAGCTGTA CTTTGTCAAG GTGGATGTGA CGGGCGCGTA 2201 CGACACCATC CCCCAGGACA GGCTCACGGA GGTCATCGCC AGCATCATCA 2251 AACCCCAGAA CACGTACTGC GTGCGTCGGT ATGCCGTGGT CCAGAAGGCC

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FIGURE 50 (cont.)

2301 GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT CTACCTTGAC 2351 AGACCTCCAG CCGTACATGC GACAGTTCGT GGCTCACCTG CAGGANAACA 2401 GCCCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG 2451 GCCAGCAGTG GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC 2501 CGTGCGCATC AGGGGCAAGT CCTACGTCCA GTGCCAGGGG ATCCCGCAGG 2551 GCTCCATCCT CTCCACGCTG CTCTGCAGCC TGTGCTACGG CGACATGGAG 2601 AACAAGCTGT TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC TGCGTTTGGT 2651 GGATGATTTC TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC 2701 TCAGGACCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACTTG 2751 CGGAAGACAG TGGTGAACTT CCCTGTAGAA GACGAGGCCC TGGGTGGCAC 2801 GGCTTTTGTT CAGATGCCGG CCCACGGCCT ATTCCCCTGG TGCGGCCTGC 2851 TGCTGGATAC CCGGACCCTG GAGGTGCAGA GCGACTACTC CAGCTATGCC 2901 CGGACCTCCA TCAGAGCCAG TCTCACCTTC AACCGCGGCT TCAAGGCTGG 2951 GAGGAACATG CGTCGCAAAC TCTTTGGGGT CTTGCGGCTG AAGTGTCACA 3001 GCCTGTTTCT GGATTTGCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC 3051 ATCTACAAGA TCCTCCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT 3101 GCAGCTCCCA TTTCATCAGC AAGTTTGGAA GAACCCCACA TTTTTCCTGC 3151 GCGTCATCTC TGACACGGCC TCCCTCTGCT ACTCCATCCT GAAAGCCAAG 3201 AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC CTCTGCCCTC 3251 CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCCTGCTC AAGCTGACTC 3301 GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACTCAG GACAGCCCAG 3351 ACGCAGCTGA GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC 3401 CGCAGCCAAC CCGGCACTGC CCTCAGACTT CAAGACCATC CTGGACTGAT 3451 GGCCACCGC CCACAGCCAG GCCGAGAGCA GACACCAGCA GCCCTGTCAC 3501 GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCCACAC CCAGGCCCGC 3551 ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT 3601 CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA 3651 GGGCTGAGTG TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG 3701 CTCGGCTCCA CCCCAGGGCC AGCTTTTCCT CACCAGGAGC CCGGCTTCCA 3751 CTCCCCACAT AGGAATAGTC CATCCCCAGA TTCGCCATTG TTCACCCCTC 3801 GCCCTGCCCT CCTTTGCCTT CCACCCCCAC CATCCAGGTG GAGACCCTGA 3851 GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG 3901 TACACAGGCG AGGACCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT 3951 GGGGGGAGGT GCTGTGGGAG TAAAATACTG AATATATGAG TTTTTCAGTT 4001 TTGAAAAAA AAAAAAAAA AAAAAAAA

FIGURE 51

	1	CCTCCCGACGCACGACGACGCCTGCACCCTTCGGGACCGGGGGCGCCTACGG	60
a b c		A A I, R P A A H V G S P C P G H P R D A · Q R C V L L R T W E A L A P A T P A M P · S A A S C C A R G K P W P R P P P R C R ·	-
	61	SCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT CGCGCGAGGGGGGACGCTCGGCACGCGAGGGACGCGTCGGTGATGGCGCTCCACGA	120
а Б С		ARSPLFSRALPAAQPLPRGA RAPRCRAVRSLLRSHYREVL ALPAAEPCAPCCAATTARCC	-
	121	GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGGCG	180
a b c		A A G H V R A A P G A P G I. A A G A A R P L A T F V R R L G P Q G W R L V Q R G R W P R S C G A W G P R A G G W C S A G	- - -
	181	GGACCCGGCGCCTTTCCGCGCGNTGGTGGCCCANTGCNTGGTGTGCGTGCCCTTGGGANGN	240
a b c		GPGGFPR?GGP??GVRALG? DPAAFRA?VÁ?C?VCVPW?? TRRLSARWWP?AWCACFG??	~
	241	ANGGENGCCCCCCCCCCCCCCCCCCCCCCCCAGGTGTCCTGCCTGAANGANCTGGTGGC TNCCCNCGCCCCCCCCCCCCCCCCCCCCCC	300
ъ Б С		? A A P R R P L L P P G V L P E ? ? G G ? ? P P A A P P S A R C P A * ? ? W W P	-
	301	CCGAGTGCTGCANANGCTGTGCGANCCCCGCGCGAANAACGTGCTGGCCTTCGGCTTCGC	360
a b c		P S A A ? A V R ? R R E ? R A G L R L R R V L ? ? T C ? R G A ? N V L A F G F A E C C ? ? C A ? A A R ? T C W P S A S R	-
	361	GCTGCTGGACGGGGCCCCCGGGGGCCCCCCGACCCTTCACCACCAGCGTGCGCAGCTA	420
a b		AAGRG PRG P R G L H H Q R A Q L L L D G A R G G P P E A F T T S V R S Y C W T G P A G A P F R P S P P A C A A T	

	421	CCACGGGTTGTGCCACTGGCTGACGCCCCCCCCCCCCCC	90
•		PAQHGDRRTAGERGVGAAAA LPNTVTDAI.RGSGAWGLLLK- CPTR*FTHCGGAGKGGCCCA-	
	481	CCGCGTGGGGGACGACGTGCTGGTTCACCTGCTGGCACGCTGCCCCNTNTTTGTCCTGGT 	340
•		PRCRRAGSPAGTLR??CAGRVGDDVLVHLLARCA?FVLVAAWATTCWFTCWHAAR?LCWW	-
	541	GENTICCCACCTICCGOCTACCANGTGTGCGGGGCCGCCGCTGTACCAGCTCGGCGCTGCNAC CCNAGGGTCGACGCGGATGGTNCACACGCCCGGGGGACATGGTCGAGCCCCGACCNTC	ნიი
;		G S Q L R L P ? V R A A A V P A R R C ? ? P S C A Y ? V C G P P L Y Q L G A A T ? ? P A A P T ? C A G R R C T S S A L ? L	-
	601	TCAGGCCCGGCCCCCGCCACACCCCTANTCCACCCCAANGCCTCTGGGATCCAACCCGCCT AGTCCGGGCCGGGCGGGGGGGGTTTGGGGATNACCTGGGCTTNCGCAGACCCCTAGGTTGCCCCGGA	650
) -		S C P A P A T R ? W T R ? R L G S N G P Q A R P P P II A ? G P E ? V W D P T G L R P G P R H T I. ? D C ? A S G I Q R A W	-
	661	GGAACCATAGCGTUAGGGAGGCCCCCCCCCCCCCCCCCCC	720
ا ن ت		G T I A S C R P C S P W A A S P G C E E E P * R Q G G R C P P G L P A P G A R R N H S V R E A G V P L G C Q P R V R G G	-
	721	GCGCCCCCCGTCACGCTCGCCTTCAGACGGCAACGCTTCTCCGGGTTCGCCACGCGACG	780
ս Ե		A R G Q C Q P K S A V A Q E A Q A W R C R G G S A S R S L P L P K R P R R G A A A G A V F A E V C R C P R G P G V A L P	-
	781	CCCTCAGCODCACCOCCACTTOCCCACCGGTCCTGGGCCCACCGGGCCAGGACGCT 	840
a b		P - A C A D A R W A G V L G F F G Q D A P E P E R T P V G Q G S W A H P G R T F L S R S G R P L G R G P G P T R A C R L	-

	E41	TGGACCGAGTGACCGTGGPTTCTGTGTGTCACCCTCCCACACCCCCCAAGAAGCCAC	900
		ACCTYS SCTCACTICSCACCAAAGACACACCACACTGGACGGTCTCGGCCCCCTTCTTCCCGTC	
•		W T E + P W F L C G V T C Q T R R R S H G P S D R G F C V V S P A R P A E E A T D R V T V V S V W C H L P D P P K K P P	
	901	CTCT*TYGGAGGGTYCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCACCA	960
· }		L F G G C A L W H A P L P P I R G F F A S L E G A L S G T R H S H P S V G R Q II L W R V R S L A R A T P T H P W A A S T	
	961	CCAO3OG3GCCCCCATCCACATCGCGGCCACCACGTCCTGGGACACGCCTTGTCCCCCGGGACAGGCCCCCGGGGGCCACCACGGGACCAGACAGACAGACCAGACAGACAGACAGACAGACCAGACAGACAGACACAGACACAGACACAGACACAGACACAGACACAGACACAGACACAGACACAGACACAGAC	1020
))		PRGPPIHIAATTSWDTFCPP HAGPPSTSRPPRPGTRLV.PF TRAFHPHRGHHVLGHALSPG	
	1021	CACATISCIGGETETRATTECTETRAGGAGATGAGGAGTCCGCTGTTCNTGTGACGCNGGGAG	1080
· · · · · · · · · · · · · · · · · · ·		V Y A E T K H F L Y S S C D K ? T A ? L C T P R P S T S S T P Q A T ? T L R P S V R R D Q A L P L L R R Q ? H C 7 P P	-
	1081	CTTOCTACTCAATATATCTGAGGCCCAGCCTGACTGGCGTTTCGGGAGGTTTCGTGGAGACA GAAGGATGAGTTATATAGACTCCGGGTCGGACTGACCGCAAGCCCTCCTGT	1140
2		L P T Q Y I * G P A * L A F G R F V E T F L L N I S E A Q P D W R S G G S W R ? S Y S I Y L R P S L T G V R E V R G D ?	-
	1141	NTCTTTCTGGTTCCAGGCCTTGGATGCCAGGATTCCCCGCAGGTTGCCCCCACCTGCCCCA	
) ;		P F L V P G L G C Q D S P Q V A P P A P S F W F Q A L D A R I P R R L P R L P Q L S G S R P W M P G F P A G C P A C P S	-
	4 204	GCGNTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAAACCACGCGCACAGTGCCC	1266
	1201	CRCNATEACCOTTTACGCCGOGGACAAAGACCTACGACGCAACCCTAGGTGCGCGTCACGGG	1.660
		APLANAAPVSGAAWEPRAVP RYWQMRFLFLELLGNHAQCP PTGKCGPCFWSCLGTTRSAF	•

		(ACTACAM DE LICE DE MANGRESE DE L'ALCE DE L'ACTACAME L'ACTACAMENTALE DE L'ACTACAMENTALISME	
	1261	CATUCCCCACAAGGAGTTCTGCGTGACGGGGGGGCTGGACGCTGGACGCTGGACGGCTGACGCTGACGGGGTGGACGCTGGACGCTGACGGGTGACGGCTGGACGGCTGGACGCTGACGCTGGACGCTGGACGCTGGACGCTGGACGCTGGACGCTGGACGCTGGACGCTGGACGCTGGACGCTGGACGCTGGACGCTGGACGCTGGACGCTGGACGCTGGACGCTGGACGCTGGACGCTGGACGACGCTGGACGCTGGACGCTGGACGCTGGACGCTGGACGCTGGACGACGCTGGACGACGCTGGACGCTGGACGACGCTGGACGACGCTGGACGACGCTGACGACGACGACGACGACGACGACGACGACGACGACGACG	1320
		L R G V P Q D A L P A A S C G H F S S R	-
i b		Y G V F L K T H C P L R A A V T F A A G -	-
c		T G C S S R R T A R C E L R S P Q Q P V -	-
		TYTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGGAGGAGAAGACACAG	380
	1321	ACAGACACGGGCCCTCTTCGGGGTCCCCGAGACACCGCCGGGGGCTCCTCCTTCTTGTTFTC	
ä		CLCPGEAPGLCGGPRGGGTQ -	-
b		V C A R E K P Q G S V A A P E E E E H P -	-
C;		S V P G R S P R A T. W R P F R R N T D -	-
		ACCCCCCTCCCTCCACCTCCTCCCCCACACACACCCCCTGCCAGGTGTACGGCT	1440
	1381	TREGGESCAGCEGACCACGTCGAGGAGGCGGTCGTGTCGTCGGGGACCGTTCCACATGCCGA	
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Э		T F V A W C S C S A S T L A P G R C T A P P P S P G A A A P P A Q Q P L A G V R L	- -
b c		PRRLVQLLRQHSSPWQVYGF	-
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i b		S C G P A C A G W C P Q A S G A F G T T P A G L P A P A G A P R P L G L Q A Q R	
Б С		V R A C L R R L V P P C L W G S R H N E	
•			
	1 501	AACGCCCCTTTCCTCAGGAACACCCAAGAGTTCATCCTCCTGGGGAAGCATGCCAAGCTCT	1560
	. 1501	${\tt TTSOSCGAAGGAGTCCTTGTGGTTCTTCAAGTAGAGGGACGCCT^{1}CGT^{2}CGT^{2}GAGA}$	
H		NAASSGTPRSSSPWGEMPSS	
þ		TPLPQEHQEVHLPGEACQAL	•
¢		RRFLRNTKKFISLGKHAKLS	-
		$\tt CGC'IVSCAGGAGC'IVGAOGTOGGAAGATGAGCGTVGCOGGACTGCGCTTVGCTVGCCAGGAGCCC$	
	1561		1620
		GCGACGTCCTCCACTGCACCTTCTACTCGCACGCCCTGACGCGAACCGACGCGTCCTCGG	
3 b		R C R S * R G R * A C G T A L G C A G A	-
Þ		A A G A D V E D E R A G L R L A A Q E P	
c:		LQELTWKMSVRDCAWLRRSP	-
		CAGGGGTTGGCTGTGTTCCGGCCGCAGAGCNCCGTCTCCGTGAGGAGATCCTGGCCAAGT	
	1521	GTCCCCAACOGACACAAGGCOGGCGTCTCGTGGCAGACGCACTCCTCTAGGACCGGTTCA	1980
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c		QSTGTRQHLKRVQLRELSEA-
		CAGAGTICAGGCAGCATGGGGAAGCCAGGCCCGGCCCTGCTGACGTCCAGACTCCGGTTCA
	1861	1920
		GICTCCACTCCCTACCCCTTCGGTCCGGGCGCGCGACTCCAGGTCTCACCCCAAGT
H		QRSGSIGKPGPPC*RPDSAS -
じ		R C Q A A S C S O A R P A D V O T F L H -
C		EVROHREARPALLTSRLRFI-
		TCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAA
	1581	
		AGGGGTTCGGACTCCGACGCCGGCTTMCACTTGTACCTGATGCAGCACCCTCGGTCTT
Ŀ		SPSLTGCGRL*TWTTSWEPE -
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c,		PKPDGLRPIVNMDYVVGART
		CETTCEGCAGAGAGAGAGAGGGCCGAGCGTCTCACCTCGAGGGTRAAGGGACTGTTCAGGG
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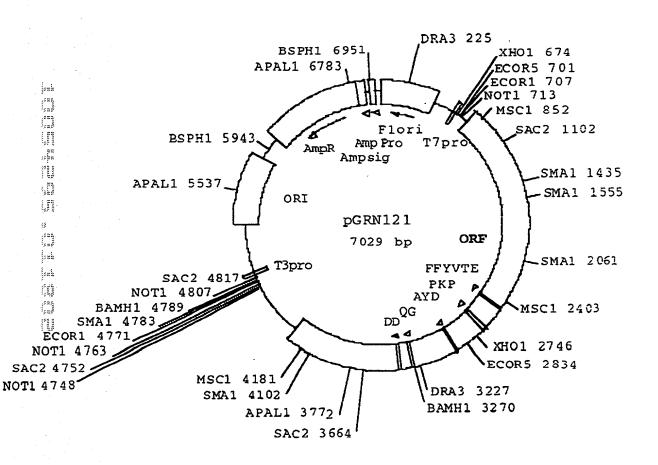
		MCPALMIC ACARDOCCI CARCACATOTI I (14) LACITACIA LA LACITACIA DE CONSTRUCCION D	2160
	2101	TECTATAGETETCCCGGACCGCGTGGAAGCACACACCACAC	2150
ā		TISTGPGAPSCCVCGPRTRR	_
b		RYPQGLAHLRAACAGPGPAA	
 خ		DIHRAWRTFVLRVRAQDEFP	
		CHCAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACA	
	2161		2220
		${\tt GACTOGACATGAAACACTTCCACCTACACTGCCGCGCGCACATGCTGTGGTAGGGGGGTCCTGT}$	
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		GCCTYLACGGAGGTCATCGCCAGCATCATCAAACCCCCAGAACACGTACTGCGTGCG	
	2221		2280
		CCGACTCCCICCAGTAGCGGTCGTAGTNGTTTGGGGTCTTGTGCATGACGCACGCAGCCA	
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c		LTEVIASIIKPONTYCVRRY	
		ATGCCGTGCTCCACAACCCCCCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCT	
	2281		2346
		TACCACCAGATCTTCCAGCACGTACCCGTGCAGGCCFTTCCAGGAAGTTCTTCGGTGCAGA	
ā		M P W S R R P P M G T S A R P S R A T S	
b		CRGPESRPWARPQGLQEPRL AVVQKAAHGHVRKAFKSHVS	
C		AVVQKAAHGHVKAFKSHVS	
		${\tt CTACCTIGACAGACCICCAGCCCCTACATCCGACAGCTTCCTGGCACCTGCAGGANAACA}$	
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	5465	GCCTCTTCCACCTCTACGCTTCATCTCCCACCACCACCTCAGCGCATCAGCGGCAAGT	
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		CCTACCTCCAGTCCCAGCCGATCCCCCAGCGCTCCATCCTCTCCACCCTGCTCCAGCC	75.4m
		GGATTECAGGTCACGGTCCCCTAGGGCGTCCCGAGGTAGGAGAGGTGCGACGAGACGTCGG	
b c		PTSSARGSRRAPSSPRCSAA LRPVPGDPAGLHTLHAALQF YVOCOGIPQGSILSTLLCSL	-
	25£1	TGT/ACTACGGGGACATGGAGAACAAGCTGTTTGCGGGGAATTCGGGGGGGACGGGCTGCTGC	2640
		ACACLEATI-CCOCTOTACCTCTTCTTCGACAAACGCCCCTAAGCCGCCCTGCCCGACGAGGG	
ā b c		C A T A T W R T S C L R G F G G T G C S V L R R H G E Q A V C G D S A G R A A P C Y G D M E N K L F A G I R R D G L L L	-
		TGCGTTTGGTGGAYGATTICTTCGTCACACCTCACCCTCACCCACGGGAAAACCTTCC	2722
	2641	ACGCAAACCACCTACTAAAGAACAACCACTYSTYGGAGTYGGGTYGGGTYGCGTYTTYGGAAGG	2700
a b c		C V W W M I S C W * H L T S P T R K P S A F G G * F L V G D T S P H T R E N L P R L V D D F L L V T P H L T H A K T F L	-
		TCAGGACCCTGGTCCCGACGTCTCCCTGAGTATGGCTGCGTGGTGGTGAACTTGCGGAAGACAG	27.52
	2/01	AGTOCTEGGACCAGGCTCCACAGGGACTCATACUGACGCACCACTTCAAACUCCTTCTGTC	2760
a b c		SCPWSEVSLSMAAW*TCGRQ QDPGPRCP*VWLRGELAE·DS FTLVRGVPEYGCVVNLRKTV	-
	2761	'IGCTCAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGG	2820
		ACCACTTGANGGGACATCTTCTGCTCCGGGACCCACCGTGCCGAAAACAAGTCTACGGCC	
ā b		W * T S L * K T R P W V A R L L F R C R G E L P C R R R G P C W H C F C S D A G V N F P V E D E A L G G T A F V Q M F A	-
	2821	CCCACGCCTATTCCCCTCGTCCGCCCTGCTGCTGGATACCCGGGACCCTGGAGGTCCACA GGGTGCCGGATAAAAAAGAGACCACGCCGGACGACCTATGGGCCCTGGGACCTCCACGTCT	2680
a b s		PTAYSPGAACCWIPGPWRCR PRPIPLVRPAAGYPDPGGAE HGLFPWCGLLLCTRTLEVQS	-
	2001	GCGACTACTCCACCTATCCCCGCACCTCCATCAGAGCCACTCTCACCTTCAACCGCCGCTCT	2940
ā b c		A T T P A M P G P P S E P V S P S T A A R L L Q L C P D L H Q S Q S H L Q P R L D Y S S Y A R T S I R A S L T F N R G F	-

	2941	TCAAGGCTGGGAACATGCGTCGCAACTCTTTTGGGGTCTTGGGGCTGAAGTGTCACA AGTTVGGACCCTTGTACGCAGCGTTTGAGAAACCCCAGAACGCGACTTCACAGTGT	3000
а Ъ С		S R L G G T C V A N S L G S C G * S V T Q G W E E H A S Q T L W G L A A E V S Q E A G R N M R R K L F G V L R L K C H S	-
	3901	CCCTCTTTCTCCATTTCCACCTCAACACCCTCCACACCCTGTCCACCCAACATCTACAACA	3060
a b		A C F W I C R * T A S R R C A F T S T R P V S G F A G E Q F P D G V H Q H L Q D L F L D L Q V N S L Q T V C T N I V K I	-
	3061	TCCTCCTCCACGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGC AGGAGGACGACGTCCGCATGTCCAAAGTGCGTACACACGACGTCGAGGGTAAAGTAGTCG	31.:0
ā b c		S S C C R R T G F T H V C C S S H F 1 S F F A A G V Q V S R M C A A A P I S S A L L L Q A Y R F H A C V L Q L P F H Q Q	-
	3121	AAGTTTWGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTC	3120
a b c		K F G R T P H F S C A S S L T R P F S A S L E E P H I F P A R H L * H G L P L 1. V W K N P T F F L R V I S D T A S L C Y	-
	3181	ACTICCATUCIGAAAGCCAACAACGCAGGGATGTCGCTGGGGGGCCAAGGGGGGCGCCCCCCCC	3240
a b c		T P S * K F R T Q G C R W G P R A F P A L H F E S Q E R R D V A G G Q G R R R P S I L K A K N A G M S L G A K C A A G P	
	3241	CTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCCAGCATTCCTGCTCAAGCTGACTC	3300
a b c		L C P P P P C S G C A T E H S C S S * L S A L R G R A V A V P P S I P A Q A D S L P S E A V Q W L C H Q A P L L K L T R	-
	3301	GACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCGCAGCTGA 	3360
a b c		D T V S P T C H S W G H S G Q F R R S * T P C H L R A T P G V T Q D S P D A A E H R V T Y V S L L G S L R T A Q T Q I. S	-

		CTOSSAAGCTCCCGGGGGACGACGCTSACTSCCCTSGAGGCCGCACCCCAACCCCACCCC	
	(36]	CASCCTTCGAGGGCCCTGCTGCGACTGACGGGACCTCCGGCCTCGCCTTGGGCCGTGACG	3420
а в С		V G F S R G R R * L P W R P Q F T R H C S E A P G D D A D C P G G R S Q P G T A R K L F G T T L T A L E A A A N P A L P	-
	3421	CCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGGCCAGGCCGAGAGCA	3480
a b		P Q T S R P S W T D G H P P T A R P R A L R L Q D H P G L M A T R P Q F G R F Q	•
<u>.</u> در		SDFKTILD * WPFAHSQAESK	-
	3481	GACACCAGCAGCCCTCTCACGCGCCCCACAC CTGTGATCCGCCGCACACTCCCCCCCCACACCCCCCCCCC	
a b		D T S S F V T P G S T S Q G G R G G P H T P A A L S R R A L R P R E G G A A H T H Q Q P C H A G L Y V P G R E G R F T F	-
	3541	CCAGGCCCGCACCGCTCGGACTCTCAGGCCTGAGTGAATGTTTTGGCCGAGGCCTGCATGT GGTCCGGGCGTGGCGACCCTCAGACTCGGGACTCACTCAC	3600
a b c		P G P H R W E S E A * V S V W P R P A C Q A R T A G S L R P E * V P G R G L H V R P A P L G V * G L S E C L A E A C M S	-
	3601	CCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGCGTGAGTGCTCCACCCAACGGCTGAGTC	3660
a b c		PAEG * V S G * G L S E C P A K C * V R L F A E C P A E A * A S V Q P R A E C G * R L S V R L R P E R V S S Q G L S V	-
	3661	TCCAGLACACCTGCCGTCTTCACTTCCCCACAGGCTGGCTCGGCTCCACCCCAGGGGCC , AGGTCGTGTCGACCGCAGAACTGAACCGCTGTCCGACCGGAGCCGAGGTGGGTTCCCGG	
きして	•	S S T P A V F T S P Q A G A R L H P R A P A H L P S S L P H R L A L G S T P G P Q H T C R L H F P T G W R S A P P Q G Q	-
	3721	AGCILITATOTO ACCACACACACACACACACACACACACACACACACACA	3780
		SFSSPGARLPLPTTETSIPE AFPHQEFGFHSPHRNSPSPD LFLTRSPASTPHIGIVHFQ7	

		THY SUCATTISTICACCCCTOSCCCTOSCCCTOCTTITISCCTTICCACCCCCACCATICCAGGIT
	3781	ANGCERTARCAAGTGGGGACCGGGACCCACGAAACGGAAGGTGGGGGGTGGTNGGTCCAC
a b c		FAIVHPSPCPPLPSTPTIQV- SFLFTPRPALLCLPPPPSRW- PHCSPLALPSPAFHPHHF5G-
		GRIZICCCIPDAGAAGGACCCCTGGGAGCTCTGGGAATTTTGGAAGTTGACCARAGGTGTGCCCCPG
		CTCT/333ACTCTTCCTGGGAQQCTICGAGACCCTTAAAQCTCACTGGTTTVCACACGGGGAC
a b c		FILERTLGALGIWSDQRCAE - PPTEGPWEIWEFGVTKGVPT - DPEKDTGSSGNLE*PKVC:FV-
	3901	TACACAGGCGAGGACCCTGCACCTGGATGGGGACTCCCTGTGGGGGGACACTCAAATTGGGGAGAGAGGT ATGTGTCCGCCCCCGGGACGGGA
а b		Y T G E D P A P G W G S T, W V K L G G C - T O A R T L H L D G G P C G S N W G E V - H R R G P C T W M C V P V G Q I G G E C
	2060	GCTGTVSGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAAA
	3341	CCACACCCTCATTTTATCACTTATATACTCAAAAAGTCAAAACTTTTTTTT
ā b c	٠	A V G V K Y * I Y E F F S F E K K K K K K K C G S K I L N I * V F Q F * K K K K K K K -
		A2AAAAAA 4029 TITTITTITT
ů		K K K -
b e		КК - кк -
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														1
GCAC	GCGC1	rgcg1	rccto	CTGC	GCAC	CGTGC	GAAC	CCCI	'GGCC	:CCGG	CCAC	CCCC	:GCG	met ATG
pro CCG	arg CGC	ala GCT	pro CCC	arg CGC	cys TGC	arg CGA	ala GCC	10 val GTG	arg CGC	ser TCC	leu CTG	leu CTG	arg CGC	ser AGC
•			20										30	
his CAC	tyr TAC	arg CGC	glu	val GTG	leu CTG	pro CCG	leu CTG	ala GCC	thr ACG	phe TTC	val GTG	arg CGG	arg CGC	leu CTG
								40						
gly GGG	pro CCC	gln CAG	gly GGC	trp TGG	arg CGG	leu CTG	val GTG	gln CAG	arg CGC	g <u>l</u> y	asp GAC	pro CCG	ala GCG	ala GCT
			50					,					60	
													trp TGG	
								70						
ala GCA	arg CGG	pro CCG	pro CCC	pro CCC	ala GCC	ala GCC	pro CCC	ser TCC	phe TTC	arg CGC	gln CAG	val GTG	ser TCC	cys TGC
·			80										90	
leu CTG	lys AAG	glu GAG	leu CTG	val GTG	ala GCC	arg CGA	val GTG	leu CTG	gln CAG	arg AGG	leu CTG	cys TGC	glu GAG	arg CGC
								100						
gly GGC	ala GCG	lys AAG	asn AAC	val GTG	leu CTG	ala GCC	phe TTC	gly GGC	phe TTC	ala GCG	leu CTG	leu CTG	asp GAC	gly GGG
			110										120	
													arg CGC	
								130						
_							_	ala	leu	_			gly	

trp TGG	gly GGG	leu CTG	140 leu CTG	leu CTG	arg CGC	arg CGC	val GTG	gly GGC	asp GAC	asp GAC	val GTG	leu CTG	150 val GTT	his CAC
	leu CTG													
ala GCC	tyr TAC	gln CAG	170 val GTG	cys TGC	gly GGG	pro CCG	pro CCG	leu CTG	tyr TAC	gln CAG	leu CTC	gly GGC	180 ala GCT	ala GCC
	gln CAG													
	gly GGA													
	pro CCC													
	ala GCC													
	ala GCC													trp TGG
	his CAC													
val GTG	val GTG	ser TCA	pro CCT	ala GCC	arg AGA	pro CCC	ala GCC	280 glu GAA	glu GAA	ala GCC	thr ACC	ser TCT	leu TTG	glu GAG

gly GGT	ala GCG	leu CTC	290 ser TCT	gly GGC	thr ACG	arg CGC	his CAC	ser TCC	his CAC	pro CCA	ser TCC	val GTG	300 gly GGC	arg CGC
gln CAG	his CAC	his CAC	ala GCG	gly GGC	pro CCC	pro CCA	ser TCC	310 thr ACA	ser TCG	arg CGG	pro CCA	pro CCA	arg CGT	pro CCC
trp TGG	asp GAC	thr ACG	320 pro CCT	cys TGT	pro CCC	pro CCG	val GTG	tyr TAC	ala GCC	glu GAG	thr ACC	lys AAG	330 his CAC	phe TTC
leu CTC	tyr TAC	ser TCC	ser TCA	gly GGC	asp GAC	lys AAG	glu GAG	340 gln CAG	leu CTG	arg CGG	pro	ser TCC	phe TTC	leu CTA
													360 leu CTC	
													thr ACT	pro CCC
														pro CCC
														gly GGG
val GTG	leu CTC	leu CTC	410 lys AAG	thr ACG	his CAC	cys TGC	pro CCG	leu CTG	arg CGA	ala GCT	ala GCG	val GTC	420 thr ACC	pro CCA
														ala GCG

			440										450	
ala GCC	prc	glu GAG	alu	glu GAG	asp GAC	thr ACA	asp GAC	CCC	arg CGT	arg CGC	leu CTG	val GTG	gln CAG	leu CTG
leu CTC	arg CGC	gln CAG	his CAC	ser AGC	ser AGC	pro CCC	trp TGG	460 gln CAG	val GTG	tyr TAC	gly	phe TTC	val GTG	arg CGG
			470										480	
ala GCC	CYS TGC	leu CTG	arg	arg CGG	leu CTG	val GTG	pro CCC	pro CCA	gly GGC	leu CTC	trp TGG	GGC ājy	ser TCC	arg AGG
								490						
his CAC	asn AAC	glu GAA	arg CGC	arg CGC	phe TTC	leu CTC	arg AGG	asn AAC	thr ACC	lys AAG	lys AAG	phe TTC	ATC	ser TCC
			500										510	
leu CTG	gly GGG	lys AAG	his CAT	ala GCC	lys AAG	leu CTC	ser TCG	leu CTG	gln CAG	glu GAG	leu CTG	thr ACG	trp TGG	lys AAG
met ATG	ser AGC	val GTG	arg CGG	asp GAC	cys TGC	ala GCT	trp TGG	520 leu CTG	arg CGC	arg AGG	ser AGC	pro CCA	gly GGG	val GTT
gly GGC	cys TGT	val GTT	530 pro CCG	ala GCC	ala GCA	glu GAG	his CAC	arg CGT	leu CTG	arg CGT	glu GAG	glu GAG	540 ile ATC	leu CTG
								550						
ala GCC	lys AAG	phe TTC	leu CTG	his CAC	trp TGG	leu CTG	met ATG	ser AGT	val GTG	tyr TAC	val GTC	val GTC	glu GAG	leu CTG
leu CTC	arg AGG	ser TCT	560 phe TTC	phe TTT	tyr TAT	val GTC	thr ACG	glu GAG	thr ACC	thr ACG	phe TTT	gln CAA	570 lys AAG	asn AAC
arg	leu	phe	phe	tyr	arg	pro	ser	580 val	trp	ser	lys	leu	gln	ser
AGG	CTC	TTT	TTC	TAC	CGG	CCG	AGT	GTC	TGG	AGC	AAG	TTG	CAA	AGC
ile ATT	gly GGA	ile ATC	590 arg AGA	gln CAG	his CAC	leu TTG	lys AAG	arg AGG	val GTG	gln CAG	leu CTG	arg CGG	600 glu GAG	leu CTG

610 ser glu ala glu val arg gln his arg glu ala arg pro ala leu TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG 630 620 leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG 640 pro ile val asn met asp tyr val val gly ala arg thr phe arg CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC 660 650 arg glu lys arg ala glu arg leu thr ser arg val lys ala leu AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG 670 phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG 680 gly ala ser val leu gly leu asp asp ile his arg ala tro arg GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC 700 thr phe val leu arg val arg ala gln asp pro pro glu leu ACC TTC GTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG 720 710 tyr phe val lys val asp val thr gly ala tyr asp thr ile pro TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC 730 gln asp arg leu thr glu val ile ala ser ile ile lys pro gln CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG 750 740 asn thr tyr cys val arg arg tyr ala val val gln lys ala ala AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC 760 his gly his val arg lys ala phe lys ser his val ser thr leu CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

									his CAC		
_									gln CAG		
			_			_	_		phe TTC		
. =									ser TCC		
									thr ACG		
_									phe TTT		gly GGG
	_							_	asp GAT	_	leu TTG
											thr ACC
		-		_					asn AAC		arg CGG
_				_		_			leu CTG		
									pro CCC		

gly GGC	leu CTG	leu CTG	leu CTG	asp GAT	thr ACC	arg CGG	thr ACC	940 leu CTG	glu GAG	val GTG	gln CAG	ser AGC	asp GAC	tyr TAC
ser TCC	ser AGC	tyr TAT	950 ala GCC	arg CGG	thr ACC	ser TCC	ile ATC	arg AGA	ala GCC	ser AGT	val GTC	thr ACČ	960 phe TTC	asn AAC
arg CGC	gly GGC	enc STT	lys AAG	ala GCT	gly GGG	arg AGG	asn AAC	970 met ATG	arg CGT	arg CGC	lys AAA	leu CTC	phe TTT	gly GGG
													990 gln CAG	
									ile				leu CTC	
				arg									102 pro CCA	phe
									phe				val GTC	
				ser									109 lys AAG	asn
									ala				leu CTG	
				gln									108 leu CTC	lys
									pro				ser TCA	

(2) 5

FIGURE 53 (cont.)

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arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr AGG ACA GCC CAG ACG CTG AGT CGG AAG CTC CCG GGG ACG ACG

1120

leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC

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